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OM protein - protein search, using sw model

Run on: October 29, 2005, 00:51:44 ; Search time 69 Seconds
(without alignments)
145.736 Million cell updates/sec

Title: US-09-980-263-1
Perfect score: 147
Sequence: 1 GMPGAGSGWEEGSGPPGVTPPLFSP 26

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	147	100.0	26	4 AAG62388	Aag62388 Alternati
2	147	100.0	26	4 AAB48914	Aab48914 Human ace
3	147	100.0	26	4 AAB50032	Aab50032 Acetylcho
4	147	100.0	26	5 AAU98024	Aau98024 Human rea
5	147	100.0	31	2 AAW74588	Aaw74588 Amino aci
6	147	100.0	31	2 AAW68146	Aaw68146 Human Ach
7	147	100.0	37	4 AAB50035	Aab50035 Acetylcho
8	147	100.0	53	4 AAB50036	Aab50036 Acetylcho
9	147	100.0	53	5 ABG31331	Abg31331 GFP-fused
10	147	100.0	600	2 AAW48797	Aaw48797 Human ace
11	63	42.9	145	7 ADC33366	Adc33366 Human nov
12	61.5	41.8	575	4 ABB11475	Abb11475 Human R31
13	61	41.5	98	3 AAB51865	Aab51865 Human sec
14	60	40.8	54	2 AAR37744	Aar37744 Collagen-
15	60	40.8	54	2 AAR93255	Aar93255 Collagen-
16	60	40.8	334	8 ADL91154	Adl91154 Mouse fic
17	60	40.8	334	8 ADL91152	Adl91152 Human fic
18	60	40.8	633	2 AAR37746	Aar37746 Collagen-
19	60	40.8	633	2 AAR93257	Aar93257 Collagen-
20	60	40.8	633	2 AAW57655	Aaw57655 Collagen-
21	60	40.8	1065	2 AAR37745	Aar37745 Collagen-
22	60	40.8	1065	2 AAR93256	Aar93256 Collagen-
23	60	40.8	1065	2 AAW57654	Aaw57654 Collagen-
24	60	40.8	1466	4 AAE02534	Aae02534 Bovine al
25	60	40.8	1466	4 AAE02533	Aae02533 Bovine al

26	59	40.1	532	2 AAW40114	Aaw40114 Human alp
27	58	39.5	226	7 ADB64162	Adb64162 Human pro
28	58	39.5	251	6 ADA54929	Ada54929 Human pro
29	58	39.5	274	8 ADQ66581	Adq66581 Novel hum
30	58	39.5	393	5 AAU86144	Aau86144 Human PRO
31	58	39.5	393	6 ADA54950	Ada54950 Human pro
32	58	39.5	393	7 ADC31141	Adc31141 Human nov
33	58	39.5	393	7 ADJ37315	Adj37315 Human tum
34	58	39.5	393	8 ADG68239	Adg68239 Human PRO
35	58	39.5	393	8 ADQ65780	Adq65780 Novel hum
36	58	39.5	421	7 ADF74163	Adf74163 Human nov
37	58	39.5	635	4 AAM78798	Aam78798 Human pro
38	58	39.5	638	5 ABJ01025	Abj01025 Human bre
39	58	39.5	638	6 ABU69146	Abu69146 Human NOV
40	58	39.5	638	8 ADO08295	Ado08295 Human NOV
41	58	39.5	644	4 AAM79782	Aam79782 Human pro
42	58	39.5	703	6 ABP96315	Abp96315 Human col
43	58	39.5	717	6 ABP96314	Abp96314 Human col
44	58	39.5	733	6 ABU69145	Abu69145 Human NOV
45	58	39.5	733	8 ADO08293	Ado08293 Human NOV

ALIGNMENTS

RESULT 1
AAG62388
ID AAG62388 standard; peptide; 26 AA.
XX AC AAG62388;
XX DT 31-AUG-2001 (first entry)
XX DE Alternately splice AChE product C-terminus AChE-R.
XX KW Antisense oligonucleotide; acetylcholine esterase; AChE; dystonia;
KW KW cholinergic neurotransmission; progressive neuromuscular disorder;
KW KW myasthenia gravis; Eaton-Lambert disease; muscular dystrophy; PTSD;
KW KW amyotrophic lateral sclerosis; post-traumatic stress disorder;
KW KW multiple sclerosis; post-stroke sclerosis; post-injury muscle damage;
XX KW excessive re-innervation.
OS Unidentified.
XX PN WO200136627-A2.
XX PD 25-MAY-2001.
XX PF 16-NOV-2000; 2000WO-IL000763.
XX PR 16-NOV-1999; 99IL-00132972.
XX PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
XX PI Soreq H, Seidman S;
XX DR WPI; 2001-336003/35.
XX PT New antisense oligonucleotide targeted to acetylcholine esterase mRNA,
XX PT useful for treating or preventing progressive neuromuscular disorders
XX PT such as myasthenia gravis.
XX PS Disclosure; Fig 1; 124pp; English.
XX CC Sequences AAH44810 - AAH44822 represent antisense oligonucleotides
XX CC targeting the acetylcholine esterase (AChE) mRNA. AChE is involved in the
XX CC termination of cholinergic neurotransmission, by hydrolysing the
XX CC neurotransmitter acetylcholine. Mammalian AChE is encoded by one gene but
XX CC alternative splicing at its 3' end yields three different mRNA
XX CC transcripts which encode protein with distinct carboxyl termini. All
XX CC three proteins are catalytically active. AChE has morphogenic, non-
XX CC catalytic capacities too. AChE antisense oligonucleotides are used in
XX CC treating or preventing a progressive neuromuscular disorder. Examples of

CC disorders which are treatable using the antisense oligonucleotides
CC include myasthenia gravis, Eaton-Lambert disease, muscular dystrophy,
CC amyotrophic lateral sclerosis, post-traumatic stress disorder (PTSD),
CC multiple sclerosis, dystonia, post-stroke sclerosis, post-injury muscle
CC damage, excessive re-innervation and post-exposure to AChE inhibitors.
CC The present sequence represents the C-terminus of an alternatively
CC spliced AChE gene product
XX
SQ Sequence 26 AA;

Query Match 100.0%; Score 147; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GMOGPAGSGWEEGSGSPPGVTPLFSP 26
Db 1 GMOGPAGSGWEEGSGSPPGVTPLFSP 26
|||||

RESULT 2
AAB48914
ID AAB48914 standard; peptide; 26 AA.
XX
AC AAB48914;
XX
DT 16-MAR-2001 (first entry)
XX
XX Human acetylcholinesterase (AChE) C-terminal peptide, SEQ ID NO:1.
DE
XX
XX Acetylcholinesterase; AChE; readthrough peptide; ARP; splice variant;
KW human; epitope; C-terminal peptide; antibody; central nervous system;
KW CNS stress; psychological insult; physical insult; chemical insult;
KW blood-brain barrier disruption; elevated glucocorticoid level;
KW Alzheimer's disease; diagnosis.
XX
XX Homo sapiens.
XX
XX WO2000073343-A2.
PN
XX
PD 07-DEC-2000.
XX
XX 31-MAY-2000; 2000WO-IL000312.
PF
XX
PR 31-MAY-1999; 99IL-00130225.
XX
XX (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
PA
XX
PI Soreq H, Kaufer D, Friedman A, Seidman S;
XX
XX WPI; 2001-061514/07.
DR
XX
XX Antibody specific to acetylcholinesterase or its C-terminal peptide
PT derivative useful for diagnosing, ventral nervous system stress, elevated
PT glucocorticoid level, disruption of blood-brain barrier and Alzheimer's
PT disease.
XX
XX Claim 4; Page 42; 44pp; English.
PS
XX
XX The invention relates to antibodies which recognise acetylcholinesterase
CC (AChE) or a C-terminal peptide thereof (particularly AAB48914-B48916).
CC The AChE splice variant, AChE-R, and AChE-R mRNA, have been found to be
CC elevated in response to central nervous system (CNS) insults. The
CC invention therefore also relates to a method for diagnosing CNS stress,
CC and also elevated glucocorticoid levels, disruption of the blood-brain
CC barrier or Alzheimer's disease using a sample (e.g., serum or
CC cerebrospinal fluid) and an antibody of the invention. The CNS stress
CC which may be diagnosed using the antibodies is preferably that caused by
CC psychological insult, physical insult (head injury, head trauma, or
CC exposure to irradiation) or chemical insult (exposure to insecticide or
CC nerve gas). The present sequence represents a human AChE C-terminal
CC peptide (termed AChE readthrough peptide (ARP) in the specification),
CC which is specifically claimed as an epitope which is recognised by an
CC antibody of the invention

XX Sequence 26 AA;
SQ

Query Match 100.0%; Score 147; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GMOGPAGSGWEEGSGSPPGVTPLFSP 26
Db 1 GMOGPAGSGWEEGSGSPPGVTPLFSP 26
|||||

RESULT 3
AAB50032
ID AAB50032 standard; peptide; 26 AA.
XX
AC AAB50032;
XX
DT 14-MAR-2001 (first entry)
XX
XX Acetylcholinesterase readthrough peptide ARP-1.
DE
XX
XX ARP-1; haemostatic; acetylcholinesterase; AChE; cell growth; human;
KW cell differentiation; thrombocytopenia; post-irradiation condition;
KW post-chemotherapy condition; blood loss; stress-induced male infertility.
XX
XX Homo sapiens.
OS
XX
XX WO2000073427-A2.
PN
XX
PD 07-DEC-2000.
XX
XX 31-MAY-2000; 2000WO-IL000311.
PF
XX
PR 31-MAY-1999; 99IL-00130224.
XX
PR 02-SEP-1999; 99IL-00131707.
XX
XX (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
PA
XX
PI Soreq H, Eldor A, Deutch V, Grisaru D;
XX
XX WPI; 2001-061523/07.
DR
XX
XX New regulatory peptides having cell growth and cell differentiation
PT activity derived from the C-terminal region of acetylcholinesterase
PT useful in promoting growth, survival and differentiation of stem cells.
XX
XX Claim 8; Page 50; 133pp; English.
PS
XX
XX The present sequence is a C-terminal peptide of acetylcholinesterase
CC (AChE). This peptide is acetylcholinesterase "readthrough" peptide (ARP-
CC 1). This peptide has a cell growth and/or cell differentiation activity.
CC The peptide may be used in ex vivo or in vivo expansion of haematopoietic
CC stem cells and neural progenitors, and in the promotion of megakaryocytic
CC differentiation of hematopoietic stem cells. In addition, the present
CC peptide may be used in for promoting expansion of committed neural
CC progenitors in a developing embryo, in cultured embryonic stem cells, and
CC embryoid bodies derived from them. The present peptide may further be
CC used in the treatment of thrombocytopenia, post-irradiation conditions,
CC post-chemotherapy conditions, and conditions following massive blood
CC loss, in inducing synthesis of AChE mRNA, and in promoting formation of
CC hematon bodies. Antibodies directed against the present peptide are
CC useful for diagnosing stress-induced male infertility
XX
SQ Sequence 26 AA;

Query Match 100.0%; Score 147; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GMOGPAGSGWEEGSGSPPGVTPLFSP 26
Db 1 GMOGPAGSGWEEGSGSPPGVTPLFSP 26
|||||

RESULT 4
AAU98024
ID AAU98024 standard; peptide; 26 AA.
XX
AC AAU98024;
XX
DT 27-AUG-2002 (first entry)
XX
DE Human readthrough acetylcholinesterase unique region.
XX
KW Human; acetylcholinesterase; single-chain variable fragment; scFv;
KW AChE-S; heavy chain variable region; muscle re-innervation;
KW progressive neuromuscular disorder; muscle distortion; readthrough;
KW myasthenia gravis; neuromuscular junction abnormality;
KW Eaton-Lambert disease; muscular dystrophy; amyotrophic lateral sclerosis;
KW ALS; post-traumatic stress disorder; PTSD; multiple sclerosis; Dystonia;
KW post-stroke sclerosis; post-injury muscle damage;
KW excessive re-innervation.
XX
OS Homo sapiens.
XX
PN WO200246422-A1.
XX
PD 13-JUN-2002.
XX
PF 22-MAY-2001; 2001WO-IL000464.
XX
PR 04-DEC-2000; 2000IL-00140071.
XX
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
XX
PI Soreq H, Flores CF, Nissim A;
XX
DR WPI; 2002-463832/49.
XX
FT Nucleic acid sequence coding for a single-chain variable fragment (scFv)
FT antibody that has specific affinity for the synaptic variant of
PT acetylcholinesterase (AChE-S), useful for diagnosing a neuromuscular
PT disorder, e.g. Myasthenia gravis.
XX
PS Disclosure; Fig 1; 73pp; English.
XX
CC The invention relates to a nucleic acid sequence coding for a single-
CC chain variable fragment (scFv) antibody that has specific affinity for
CC the synaptic variant of acetylcholinesterase (AChE-S), where the scFv
CC antibody consists essentially of a polypeptide comprising the binding
CC portion of the heavy chain variable region of an antibody. Also included
CC are an expression vehicle comprising a nucleic acid sequence coding for a
CC scFv antibody that has specific affinity for the synaptic variant of AChE
CC -S, an scFv antibody specifically recognising and binding to the synaptic
CC variant of AChE-S and a method for the diagnosis of a progressive
CC neuromuscular disorder in a mammal, comprising obtaining a sample from
CC the mammal and detecting intensified expression of at least one of the
CC AChE variants in the sample. The single-chain Fv antibody is useful for
CC diagnosing a progressive neuromuscular disorder which involves any one of
CC muscle distortion, muscle re-innervation and neuromuscular junction (NMJ)
CC abnormalities. The disorder is Myasthenia gravis (preferred), Eaton-
CC Lambert disease, muscular dystrophy, amyotrophic lateral sclerosis (ALS),
CC post-traumatic stress disorder (PTSD), multiple sclerosis, Dystonia, post
CC -stroke sclerosis, post-injury muscle damage, excessive re-innervation,
CC or post-exposure to AChE inhibitors. The present sequence represents the
CC unique region of human acetylcholinesterase encoded by a readthrough
XX splice variant
SQ Sequence 26 AA;

Query Match 100.0%; Score 147; DB 5; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GMSGPAGSGWEEGSGPPGVTPLEFSP 26

QY 1 GMSGPAGSGWEEGSGPPGVTPLEFSP 26

Db 1 GMSGPAGSGWEEGSGPPGVTPLEFSP 26
RESULT 5
AAW74588
ID AAW74588 standard; protein; 31 AA.
XX
AC AAW74588;
XX
DT 21-DEC-1998 (first entry)
XX
DE Amino acid sequence of the human AChE variant 7.
XX
KW Nuclease resistance; inhibition; human; acetyl-cholinesterase; AChE;
KW central nervous system; CNS.
XX
OS Homo sapiens.
XX
PN WO9839486-A1.
XX
PD 11-SEP-1998.
XX
PF 06-MAR-1998; 98WO-US004503.
XX
PR 06-MAR-1997; 97US-0040203P.
XX
PA (YISS) YISSUM RES & DEV CO.
PA (KOHN/) KOHN K I.
XX
PI Soreq H, Seidman S, Shohami E;
XX
DR WPI; 1998-506377/43.
XX
PT Treatment of injury to central nervous system - by administration of
PT inhibitor of acetyl-cholinesterase production.
XX
PS Disclosure; Page 62; 88pp; English.
XX
CC This is the amino acid sequence of a human acetyl-cholinesterase (AChE)
CC variant used in the method of the invention, where inhibitors of AChE are
CC used to treat injury to the central nervous system (CNS). The AChE
CC inhibitor can also be used to facilitate transplantation of neuronal
CC cells to the CNS of a patient. The inhibitor can also be used to improve
CC hippocampal neuron survival following injury to the CNS. The CNS injuries
CC that can be treated with the method include epilepsy, stroke,
CC Huntington's disease, head injury, spinal injury, pain, Parkinson's
CC disease, myelin deficiencies, neuromuscular disorders, neurological pain,
CC amyotrophic lateral sclerosis, Alzheimer's disease, and affective
CC disorders of the brain.
XX
SQ Sequence 31 AA;

Query Match 100.0%; Score 147; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.6e-10;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GMSGPAGSGWEEGSGPPGVTPLEFSP 26
6 GMSGPAGSGWEEGSGPPGVTPLEFSP 31

QY 1 GMSGPAGSGWEEGSGPPGVTPLEFSP 26
Db 6 GMSGPAGSGWEEGSGPPGVTPLEFSP 31
RESULT 6
AAW68146
ID AAW68146 standard; protein; 31 AA.
XX
AC AAW68146;
XX
DT 05-OCT-1998 (first entry)
XX
DE Human AChE splice variant E1-4-I4-E5.
XX
KW Nuclease resistant; acetylcholinesterase; human; myasthenia gravis; AChE;

KW Parkinson's disease; Alzheimer's disease; central nervous system;
XX neuromuscular junction; cholinergic signalling; brain.

OS Homo sapiens.

XX WO9826062-A2.

XX 18-JUN-1998.

XX 12-DEC-1997; 97WO-US023598.

XX 12-DEC-1996; 96US-0035266P.

XX 13-FEB-1997; 97US-0037777P.

XX 02-MAY-1997; 97US-00850347.

XX 21-JUL-1997; 97US-0053334P.

XX (YISS) YISSUM RES & DEV CO.

XX (KOHN/) KOHN K I.

XX Soreq H, Seidman S, Eckstein F, Friedman A, Kaufer D;

XX WPI; 1998-348522/30.

XX Synthetic nuclease resistant antisense oligodeoxynucleotides - directed

XX against acetylcholinesterase, useful for treating Parkinson's and

XX Alzheimer's diseases and myasthenia gravis.

XX Disclosure; Fig 12; 89pp; English.

XX This represents the amino acid sequence of a human acetylcholinesterase

XX (AChE) splice variant. The invention provides sequences shown in AAV41278

XX to AAV41285 that represent synthetic nuclease resistant antisense

XX oligodeoxynucleotides which are capable of selectively modulating human

XX acetylcholinesterase (AChE) production. These oligonucleotides are

XX targeted to a splice junction in a splice variant of AChE mRNA and are

XX capable of selectively modulating human AChE production in the central

XX nervous system and neuromuscular junction. The invention also provides a

XX method for determining the efficacy of these human AChE specific

XX antisense oligonucleotides. These antisense oligonucleotides can be used

XX to restore balanced cholinergic signalling in the brain, particularly

XX related to learning and memory as well as stress disorders, Parkinson's

XX and Alzheimer's disease. They can also be used to reduce production and

XX therefore deposition of AChE in the neuromuscular junctions of patients

XX with e.g. myasthenia gravis. The oligonucleotides work effectively at low

XX doses while avoiding many of the side effects associated with Tacrine and

XX related cholinergic drugs for Alzheimer's disease and pyridostigmine and

XX related drugs for myasthenia gravis

XX Sequence 31 AA;

XX Query Match 100.0%; Score 147; DB 2; Length 31;

XX Best Local Similarity 100.0%; Pred. No. 1.6e-10;

XX Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OS Homo sapiens.

XX WO200073427-A2.

XX 07-DEC-2000.

XX 31-MAY-2000; 2000WO-IL000311.

XX 31-MAY-1999; 99IL-00130224.

XX 02-SEP-1999; 99IL-00131707.

XX (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.

XX Soreq H, Eldor A, Deutch V, Grisaru D;

XX WPI; 2001-061523/07.

XX New regulatory peptides having cell growth and cell differentiation

XX activity derived from the C-terminal region of acetylcholinesterase

XX useful in promoting growth, survival and differentiation of stem cells.

XX Example 10; Page 76; 133pp; English.

XX The present invention relates to C-terminal peptides of

XX acetylcholinesterase (AChE) (see AAB50032-B50034). The peptides of the

XX present invention have cell growth and/or cell differentiation activity.

XX The peptides may be used in ex vivo or in vivo expansion of

XX haematopoietic stem cells and neural progenitors, and in the promotion of

XX megakaryocytic differentiation of hematopoietic stem cells. In addition,

XX the peptides may be used in for promoting expansion of committed neural

XX progenitors in a developing embryo, in cultured embryonic stem cells, and

XX embryoid bodies derived from them. The peptides may further be used in

XX the treatment of thrombocytopenia, post-irradiation conditions, post-

XX chemotherapy conditions, and conditions following massive blood loss, in

XX inducing synthesis of AChE mRNA, and in promoting formation of hematoma

XX bodies. Antibodies directed against the peptides are useful for

XX diagnosing stress-induced male infertility. The present sequence is a C-

XX terminal AChE "readthrough" peptide (ARP-2)

XX Sequence 37 AA;

XX Query Match 100.0%; Score 147; DB 4; Length 37;

XX Best Local Similarity 100.0%; Pred. No. 1.9e-10;

XX Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GMOGPAGSGWEEGSGSPPGVTPLFSP 26

DB 12 GMOGPAGSGWEEGSGSPPGVTPLFSP 37

RESULT 8

AAB50036

ID AAB50036 standard; protein; 53 AA.

XX AAB50036;

XX 14-MAR-2001 (first entry)

XX Acetylcholinesterase protein #1 used in a yeast two-hybrid system.

KW Parkinson's disease; Alzheimer's disease; central nervous system;
XX neuromuscular junction; cholinergic signalling; brain.

OS Homo sapiens.

XX WO9826062-A2.

XX 18-JUN-1998.

XX 12-DEC-1997; 97WO-US023598.

XX 12-DEC-1996; 96US-0035266P.

XX 13-FEB-1997; 97US-0037777P.

XX 02-MAY-1997; 97US-00850347.

XX 21-JUL-1997; 97US-0053334P.

XX (YISS) YISSUM RES & DEV CO.

XX (KOHN/) KOHN K I.

XX Soreq H, Seidman S, Eckstein F, Friedman A, Kaufer D;

XX WPI; 1998-348522/30.

XX Synthetic nuclease resistant antisense oligodeoxynucleotides - directed

XX against acetylcholinesterase, useful for treating Parkinson's and

XX Alzheimer's diseases and myasthenia gravis.

XX Disclosure; Fig 12; 89pp; English.

XX This represents the amino acid sequence of a human acetylcholinesterase

XX (AChE) splice variant. The invention provides sequences shown in AAV41278

XX to AAV41285 that represent synthetic nuclease resistant antisense

XX oligodeoxynucleotides which are capable of selectively modulating human

XX acetylcholinesterase (AChE) production. These oligonucleotides are

XX targeted to a splice junction in a splice variant of AChE mRNA and are

XX capable of selectively modulating human AChE production in the central

XX nervous system and neuromuscular junction. The invention also provides a

XX method for determining the efficacy of these human AChE specific

XX antisense oligonucleotides. These antisense oligonucleotides can be used

XX to restore balanced cholinergic signalling in the brain, particularly

XX related to learning and memory as well as stress disorders, Parkinson's

XX and Alzheimer's disease. They can also be used to reduce production and

XX therefore deposition of AChE in the neuromuscular junctions of patients

XX with e.g. myasthenia gravis. The oligonucleotides work effectively at low

XX doses while avoiding many of the side effects associated with Tacrine and

XX related cholinergic drugs for Alzheimer's disease and pyridostigmine and

XX related drugs for myasthenia gravis

XX Sequence 31 AA;

XX Query Match 100.0%; Score 147; DB 2; Length 31;

XX Best Local Similarity 100.0%; Pred. No. 1.6e-10;

XX Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OS Homo sapiens.

XX WO200073427-A2.

XX 07-DEC-2000.

XX 31-MAY-2000; 2000WO-IL000311.

XX 31-MAY-1999; 99IL-00130224.

XX 02-SEP-1999; 99IL-00131707.

XX (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.

XX Soreq H, Eldor A, Deutch V, Grisaru D;

XX WPI; 2001-061523/07.

XX New regulatory peptides having cell growth and cell differentiation

XX activity derived from the C-terminal region of acetylcholinesterase

XX useful in promoting growth, survival and differentiation of stem cells.

XX Example 10; Page 76; 133pp; English.

XX The present invention relates to C-terminal peptides of

XX acetylcholinesterase (AChE) (see AAB50032-B50034). The peptides of the

XX present invention have cell growth and/or cell differentiation activity.

XX The peptides may be used in ex vivo or in vivo expansion of

XX haematopoietic stem cells and neural progenitors, and in the promotion of

XX megakaryocytic differentiation of hematopoietic stem cells. In addition,

XX the peptides may be used in for promoting expansion of committed neural

XX progenitors in a developing embryo, in cultured embryonic stem cells, and

XX embryoid bodies derived from them. The peptides may further be used in

XX the treatment of thrombocytopenia, post-irradiation conditions, post-

XX chemotherapy conditions, and conditions following massive blood loss, in

XX inducing synthesis of AChE mRNA, and in promoting formation of hematoma

XX bodies. Antibodies directed against the peptides are useful for

XX diagnosing stress-induced male infertility. The present sequence is a C-

XX terminal AChE "readthrough" peptide (ARP-2)

XX Sequence 37 AA;

XX Query Match 100.0%; Score 147; DB 4; Length 37;

XX Best Local Similarity 100.0%; Pred. No. 1.9e-10;

XX Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GMOGPAGSGWEEGSGSPPGVTPLFSP 26

DB 12 GMOGPAGSGWEEGSGSPPGVTPLFSP 37

RESULT 8

AAB50036

ID AAB50036 standard; protein; 53 AA.

XX AAB50036;

XX 14-MAR-2001 (first entry)

XX Acetylcholinesterase protein #1 used in a yeast two-hybrid system.

PR 02-SEP-1999; 99IL-00131707.
XX (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
PA Soreq H, Eldor A, Deutch V, Grisaru D;
XX WPI; 2001-061523/07.
DR New regulatory peptides having cell growth and cell differentiation
XX activity derived from the C-terminal region of acetylcholinesterase
XX useful in promoting growth, survival and differentiation of stem cells.
PT Claim 8; Page 87; 133pp; English.
PT The present invention relates to C-terminal peptides of
XX acetylcholinesterase (AChE) (see AAB50032-B50034). The peptides of the
XX present invention have cell growth and/or cell differentiation activity.
XX The peptides may be used in ex vivo or in vivo expansion of
XX haematopoietic stem cells and neural progenitors, and in the promotion of
XX megakaryocytic differentiation of hematopoietic stem cells. In addition,
XX the peptides may be used in for promoting expansion of committed neural
XX progenitors in a developing embryo, in cultured embryonic stem cells, and
XX embryoid bodies derived from them. The peptides may further be used in
XX the treatment of thrombocytopenia, post-irradiation conditions, post-
XX chemotherapy conditions, and conditions following massive blood loss, in
XX inducing synthesis of AChE mRNA, and in promoting formation of hematon
XX bodies. Antibodies directed against the peptides are useful for
XX diagnosing stress-induced male infertility. The present sequence is a C-
XX terminal AChE "readthrough" protein (ARP), which was used in a yeast two-
XX hybrid system, to screen for ARP binding partners
SQ Sequence 53 AA;

Query Match 100.0%; Score 147; DB 4; Length 53;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GMOGPAGSGWEEGSGSPGVTPLFSP 26
DB 28 GMOGPAGSGWEEGSGSPGVTPLFSP 53

RESULT 9
ABG31331
ID ABG31331 standard; protein; 53 AA.
XX
AC ABG31331;
XX
DT 05-NOV-2002 (first entry)
XX
DE GFP-fused AChE variant expression construct, pGARP related protein.
XX Nervous system; drug assay; acetylcholinesterase; AChE; brain;
KW isoform variance; AChE blocker; muscarinic receptor; M1; M2;
KW pyridostigmine; muscarinic receptor blocker; scopolamine;
KW M1 receptor blocker; pirenzepine; anxiety; post-traumatic stress;
KW Alzheimer's disease; muscle malfunctioning; neurodegenerative disorder;
KW xenobiotic damage; panic; neuromuscular disorder; Parkinson's disease;
KW Huntington's chorea; muscle fatigue; multiple chemical sensitivity;
KW autism; multiple sclerosis; Sjogren's disease; GFP; pGARP;
KW green fluorescent protein.
XX Unidentified.
OS
XX WO200240994-A2.
PN
XX 23-MAY-2002.
PD
XX 14-NOV-2001; 2001WO-IL001051.
XX
XX 14-NOV-2000; 2000US-0247970P.
PR
XX (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
PA

XX Soreq H, Meshorer E, Sklan E, Shoham S;
PI WPI; 2002-490152/52.
XX
XX Evaluating effect of drugs on nervous system by comparing effect of drug
PT on acetylcholinesterase, AChE activity in brain of test animal following
PT challenge by AChE blocker and comparing it with control group.
XX Example; Page 52; 114pp; English.
PS The present invention relates to a method and system for evaluating an
XX effect on the nervous system of a test drug. The method comprises
XX comparing the effect of the drug on acetylcholinesterase (AChE) catalytic
XX activity or isoform variance in a brain of a test animal following a
XX challenge by an AChE blocker or a blocker of AChE and muscarinic
XX receptors M1 and M2 (e.g. pyridostigmine) and comparing this effect with
XX that of a known agent, preferably a non-selective muscarinic receptor
XX blocker (e.g. scopolamine) or a specific M1 receptor blocker (e.g.
XX pirenzepine). The method is useful for evaluating an effect on the
XX nervous system of a test drug, including drugs for the treatment of
XX anxiety conditions, post-traumatic stress, Alzheimer's disease, muscle
XX malfunctioning, neurodegenerative disorders, damage resulting from
XX exposure to xenobiotics, panic, neuromuscular disorders, Parkinson's
XX disease, Huntington's chorea, muscle fatigue, multiple chemical
XX sensitivity, autism, multiple sclerosis and Sjogren's disease. The
XX present sequence represents a protein described in relation to green
XX fluorescent protein (GFP)-fused AChE variant expression construct pGARP
XX in the examples of the present invention
SQ Sequence 53 AA;

Query Match 100.0%; Score 147; DB 5; Length 53;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GMOGPAGSGWEEGSGSPGVTPLFSP 26
DB 28 GMOGPAGSGWEEGSGSPGVTPLFSP 53

RESULT 10
AAW48797
ID AAW48797 standard; protein; 600 AA.
XX
AC AAW48797;
XX
DT 07-OCT-1998 (first entry)
XX
DE Human acetylcholine esterase-I4 readthrough splice variant.
XX
KW Human acetylcholine esterase-I4 readthrough splice variant; AChE-I4; CNS;
KW blood/brain barrier; BBB; I4 peptide; antibiotic; brain tumour; glioma;
KW chemotherapeutic drug; central nervous system.
XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT Region 1..574
FT /note= "This region is encoded by exons 1-4 of AChE"
FT 575..599
FT /note= "I4 peptide encoded by intron 4 of AChE; this
FT sequence is claimed by the inventors under claim 2 in the
FT specification"
FT 600
FT /note= "residue encoded by exon 5 of AChE"
XX
PN WO98222132-A2.
XX
PD 28-MAY-1998.
XX
XX 20-NOV-1997; 97WO-US021696.
XX

PR 20-NOV-1996; 96US-00311194P.
PR 12-DEC-1996; 96US-0035266P.
PR 21-JUL-1997; 97US-0053200P.
XX (YISS) YISSUM RES & DEV CO.
PA (KOHN/) KOHN K I.
XX Soreq H, Friedman A, Seidman S, Kaufer D;
PI WPI; 1998-312172/27.
XX
XX Increasing the permeability of the blood/brain barrier - using e.g.
PT adrenaline, atropine or acetylcholine esterase I4 splice variant peptide,
PT useful for imaging and/or treatment of central nervous system disorders.
XX
XX Claim 1, 2; Page 45; 71pp; English.
PS
XX The present sequence represents human acetylcholine esterase-I4 (AChE-I4)
CC readthrough splice variant. The protein sequence comprises residues
CC encoded by exons 1-4 of human AChE followed by residues encoded by intron
CC 4, while the last residue of the protein is encoded by exon 5 of AChE.
CC The invention provides a pharmaceutical composition, for facilitating
CC passage of compounds through the blood/brain barrier (BBB), comprising of
CC AChE-I4, I4 peptide or AChE-I4 analogues together with a pharmaceutically
CC acceptable carrier. The pharmaceutical composition is claimed to
CC facilitate a reversible disruption of the BBB allowing transport of
CC compounds through the BBB. The compounds, e.g. imaging agents,
CC antibiotics or chemotherapeutic drugs, are claimed to be useful for the
CC diagnosis and treatment of diseases or disorders of the CNS such as
CC infections, neurochemical disorders, brain tumours, gliomas, etc
XX
SQ Sequence 600 AA;
Query Match 100.0%; Score 147; DB 2; Length 600;
Best Local Similarity 100.0%; Pred. No. 3.2e-09;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GMOGPAGSGWEEGSGSPPGVTPLFSP 26
DB 575 GMOGPAGSGWEEGSGSPPGVTPLFSP 600
RESULT 11
ADC33366
ID ADC33366 standard; protein; 145 AA.
XX
AC ADC33366;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human novel contig-encoded polypeptide sequence, SEQ ID NO:3448.
DE
XX Human; diagnostic; drug screening; forensics; gene mapping;
KW biodiversity assessment; Parkinson's disease; Alzheimer's disease;
KW neurodegenerative diseases; anaemia; platelet disorder; wound; burns;
KW ulcers; osteoporosis; autoimmune disease; cancer;
KW molecular weight marker; food supplement; antiparkinsonian; nootropic;
KW neuroprotective; antianaemic; anticoagulant; thrombolytic; vulnerary;
KW antiulcer; osteopathic; immunosuppressive; antiinflammatory; cytostatic;
KW gene therapy.
XX
OS Homo sapiens.
XX
PN WO2003029271-A2.
XX
PD 10-APR-2003.
XX
XX 24-SEP-2002; 2002WO-US030474.
PF
XX 24-SEP-2001; 2001US-0324631P.
PR
XX (HYSE-) HYSEQ INC.
PA
XX

PI Tang TY, Zhang J, Ren F, Xue AJ, Zhao QA, Wang J, Wehrman T;
PI Zhou P, Ghosh M, Wang D, Ma Y, Asundi V, Wang Z, Weng G;
PI Haley-Vicente D, Drmanac RT;
XX
DR WPI; 2003-371981/35.
DR N-PSDB; ADC32599.
XX
PT New polynucleotide and polypeptide useful for diagnosing, preventing or
PT treating conditions such as neurodegenerative diseases, anemias, platelet
PT disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
PT cancer.
XX
PS Example 2; SEQ ID NO 3448; 1185pp; English.
XX
CC The invention relates to 971 novel human cDNA sequences (ADC29919-
CC ADC30889) and the polypeptides they encode (ADC30890-ADC31860). The
CC invention also relates to nucleic acid sequences over 99% identical with
CC the novel human cDNAs. The invention additionally encompasses expression
CC vectors and host cells comprising a nucleic acid of the invention; the
CC recombinant production of a polypeptide of the invention; an antibody
CC against a polypeptide of the invention; a method of detecting
CC polynucleotides or polypeptides of the invention; and methods of
CC identifying a compound which binds to a polypeptide of the invention. The
CC invention further discloses methods of preventing, treating or
CC ameliorating a medical condition; kits comprising polynucleotide probes
CC and/or monoclonal antibodies for carrying out the methods of the
CC invention; methods for the identification of compounds that modulate the
CC expression or activity of the polynucleotide and/or polypeptide; and 767
CC contig sequences corresponding to the cDNA sequences of the invention
CC (ADC31861-ADC32627) and the polypeptides encoded by the contigs (ADC32628
CC -ADC33394). The nucleic acids and polypeptides of the invention are
CC useful in diagnostics, drug screening, forensics, gene mapping, in the
CC identification of mutations responsible for genetic disorders or other
CC traits, for assessing biodiversity, and in producing many other types of
CC data and products dependent on DNA and amino acid sequences. They are
CC also used for treating diseases such as Parkinson's disease, Alzheimer's
CC disease and other neurodegenerative diseases, anaemia, platelet
CC disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
CC cancer. The nucleic acids may also be used as hybridisation probes or
CC primers, and in the recombinant production of a protein. The polypeptides
CC are also useful in generating antibodies, as molecular weight markers,
CC and as food supplements. The present sequence represents a human contig-
CC encoded polypeptide sequence used in an example of the invention. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 145 AA;
Query Match 42.9%; Score 63; DB 7; Length 145;
Best Local Similarity 54.2%; Pred. No. 8.7;
Matches 13; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
QY 3 QGPAGSGWEEGSGSPPGVTPLFSP 26
DB 71 QGDRGTEGKEGSGSPPGTAGMWP 94
RESULT 12
ABB11475
ID ABB11475 standard; peptide; 575 AA.
XX
AC ABB11475;
XX
XX
DT 11-JAN-2002 (first entry)
XX
DE Human R31449_3 homologue, SEQ ID NO:1845.
XX
KW Human; cytokine; cell proliferation; cell differentiation; growth factor;
KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
KW inhibitor; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
KW

CC increase or decrease storage capabilities, fat content, lipid, protein,
CC carbohydrate, vitamins, minerals, cofactors and other nutritional
CC components. Oligonucleotides AAC93470 - AAC93478 and peptide AAB51826 are
CC used in the isolation and characterisation of the proteins and
CC polynucleotides of the invention
XX
SQ Sequence 98 AA;

Query Match 41.5%; Score 61; DB 3; Length 98;
Best Local Similarity 59.1%; Pred. No. 10;
Matches 13; Conservative 0; Mismatches 7; Indels 2; Gaps 1;

QY 5 PACSGWEEGSGSPPGVTPLESP 26
| | | | | | | | | | | | | | | | | |
Db 64 PRSGWERAPGCP--VTPLTLP 83

RESULT 14
AAR37744
ID AAR37744 standard; protein; 54 AA.
XX
AC AAR37744;

XX
DT 25-MAR-2003 (revised)
DT 07-SEP-1993 (first entry)

XX
DE Collagen-like polymer DCP-(DB)3.

XX
KW Recombinant; collagen-like polymer; CLP; tripeptide; helix; membrane;
KW fibre; film; coating; triad sequence; collagen; mammalian; moulding;
KW hydrogel; interchain linkage; colloid suspension; DCP; antibody.

XX
OS Synthetic.

XX
PN WO9310154-A1.

XX
PD 27-MAY-1993.

XX
PF 04-NOV-1992; 92WO-US009485.

XX
PR 12-NOV-1991; 91US-00791960.

XX
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.

XX
PI Cappello J, Ferrari FA;

XX
WPI; 1993-182496/22.

DR
N-PSDB; AAQ43035.

XX
PT High mol. wt. collagen-like protein polymers - capable of being produced
PT in unicellular microorganisms.

XX
PS Disclosure; Page 52; 82pp; English.

XX
CC The sequences given in AAR37744 and AAR37747 represent examples of
CC recombinantly produced DCP collagen-like polymers (CLPs) which consist of
CC repeated tripeptide sequences selected from a wide range of GXY
CC sequences, where X and Y can be any amino acid. The DNA encoding these
CC sequences can be cloned into plasmids and used to transform E. coli to
CC produce the DCP proteins. DCP peptides comprise repeated units of; B =
CC GSRGDPGPP, C = GAHGPAGPK and/or D = GAQGPAGPG. These polymers have
CC molecular weights of >30 kD and are able to form helices due to
CC interchain linkages. These polymers pref. contain a proportion of
CC tripeptide triad sequences found in natural collagens, pref. mammalian
CC collagens. The CLPs impart unique characteristics to materials such as
CC fibres, membranes, films, coatings, hydrogels, colloid suspensions and
CC moulded articles. (Updated on 25-MAR-2003 to correct PN field.)

XX
SQ Sequence 54 AA;

Query Match 40.8%; Score 60; DB 2; Length 54;
Best Local Similarity 57.9%; Pred. No. 7.3;
Matches 11; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 GMOGPAGSGWEEGSGSPPG 19
| | | | | | | | | | | | | | | | | |
Db 1 GAQGPAGPGGSRGDPGPPG 19

RESULT 15

AAR93255

ID AAR93255 standard; protein; 54 AA.

XX
AC AAR93255;

XX
DT 25-MAR-2003 (revised)

DT 24-FEB-1997 (first entry)

XX
DE Collagen-like polymer sequence D4/D5 unit (DB)3.

XX
KW collagen; repetitive triad motif; recombinant production; photographic;
KW medical; structural; fibre.

XX
OS Synthetic.

XX
PN US5496712-A.

XX
PD 05-MAR-1996.

XX
PF 05-NOV-1992; 92US-00972032.

XX
PR 06-NOV-1990; 90US-00609716.

PR 12-NOV-1991; 91US-00791960.

XX
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.

XX
PI Cappello J, Ferrari FA;

XX
WPI; 1996-150728/15.

DR
N-PSDB; AAT16769.

XX
PT Collagen-like polymers comprising repetitive triads - produced in
PT unicellular organisms with improved characteristics, useful in, e.g.
PT photographic and medical fibres.

XX
PS Example 3; Col 23-24; 43pp; English.

XX
CC The invention concerns collagen-like polymers having repetitive triads
CC with reduced proline content, and where glycine is the initial amino acid
CC and the subsequent amino acids are varied. The choice of triads utilised
CC in a recombinant collagen-like polymer are chosen in order to affect
CC properties such as helix stability, hydration, solubility, gel point,
CC biodegradation and immunogenicity. Triads of particular interest include
CC GAP, GPA, GPP, GAS, GPG, GPS, GAQ, GSP, GLQ, GPR, GPK, GAK, GAR, GER,
CC GDR, GEP, GDA, GAH and GEA. The collagen-like polymers may impart new
CC characteristics, finding wide used in photographic, medical, structural
CC and fibre applications, and are capable of being produced in unicellular
CC microorganisms at high mol. wts. and in high efficiency. The present
CC sequence, encoded by clone pPT0224 (see AAT16769), was identified to
CC contain the Sequenced gene 4 or 5 monomer sequence (DB)3. The Sequenced
CC collagen-like polymers are used as immunogens for the prepn. of
CC antibodies. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-
CC MAR-2003 to correct PA field.)

XX
SQ Sequence 54 AA;

Query Match 40.8%; Score 60; DB 2; Length 54;
Best Local Similarity 57.9%; Pred. No. 7.3;
Matches 11; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 GMOGPAGSGWEEGSGSPPG 19
| | | | | | | | | | | | | | | | | |

Db 1 GAQGPAGPGGSRGDPGPPG 19

Search completed: October 29, 2005, 01:03:13

Job time : 74 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 29, 2005, 00:54:48 ; Search time 16 Seconds
(without alignments)
156.352 Million cell updates/sec

Title: US-09-980-263-1
Perfect score: 147
Sequence: 1 GMSGAGSGWEGSGSPPGVTPLFSP 26

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	60	40.8	334	2 JC5980	ficolin-A precursor
2	60	40.8	1049	1 CGB07S	collagen alpha 1(I
3	58.5	39.8	72	2 I53411	acetylcholines
4	58.5	39.8	1076	2 JC2217	major surface glyc
5	58	39.5	591	2 A84765	hypothetical prote
6	58	39.5	888	2 S28791	collagen alpha 1(X
7	58	39.5	1464	2 S59856	collagen alpha 1(I
8	57	38.8	317	2 T19143	hypothetical prote
9	57	38.8	635	2 A57131	collagen alpha 2(V
10	57	38.8	1366	1 CGHU2S	collagen alpha 2(I
11	56	38.1	282	2 JS0168	collagen col-8 - C
12	56	38.1	282	2 T16036	cuticle collagen c
13	56	38.1	325	2 T18594	hypothetical prote
14	56	38.1	920	2 B34493	collagen alpha 1(I
15	56	38.1	1373	1 A43291	collagen alpha 2(I
16	56	38.1	3198	2 A43426	collagen alpha 2 f
17	55.5	37.8	1712	1 CGHU2B	collagen alpha 2(I
18	55	37.4	316	2 T19288	hypothetical prote
19	55	37.4	439	2 D70954	hypothetical glyci
20	55	37.4	469	2 A24450	collagen alpha 2(V
21	55	37.4	633	2 B40983	collagen alpha 1(X
22	55	37.4	886	2 I50694	collagen alpha 1(I
23	55	37.4	1453	2 S21626	collagen alpha 1(I
24	55	37.4	1466	1 CGHU7L	collagen alpha 1(I
25	55	37.4	1761	2 T13990	collagen type IV a
26	54	36.7	316	2 T19291	hypothetical prote
27	54	36.7	1051	2 A35763	collagen alpha 2 c
28	54	36.7	1142	2 JX0369	collagen alpha 1(X
29	54	36.7	1418	2 T45467	collagen alpha 1(I

30	54	36.7	1419	2 A41182	collagen alpha 1(I
31	54	36.7	1487	1 CGHU6C	collagen alpha 1(I
32	54	36.7	1487	2 B41182	collagen alpha 1(I
33	54	36.7	1549	2 I48103	type VII collagen
34	54	36.7	1573	2 S01845	DNA (cytosine-5)-
35	54	36.7	1669	1 CGHU4B	collagen alpha 1(I
36	54	36.7	1669	1 CGMS4B	collagen alpha 1(I
37	53.5	36.4	608	2 A35021	myosin-light-chain
38	53	36.1	107	2 B61396	collagen alpha 1(I
39	53	36.1	187	2 A35980	collagen alpha 1(I
40	53	36.1	325	2 S02170	collagen alpha 1(I
41	53	36.1	325	2 T16324	hypothetical prote
42	53	36.1	564	2 T49322	related to RNA-bin
43	53	36.1	921	2 S40495	collagen alpha 1(I
44	53	36.1	921	2 S42617	collagen alpha 1(I
45	53	36.1	931	2 S13580	collagen alpha 1(I

ALIGNMENTS

RESULT 1

JC5980
C;Species: Mus musculus (house mouse)
C;Date: 06-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: JC5980
R;Fujimori, Y.; Harumiya, S.; Fukumoto, Y.; Miura, Y.; Yagasaki, K.; Tachikawa, H.; Fuji
Biochem. Biophys. Res. Commun. 244, 796-800, 1998
A;Title: Molecular cloning and characterization of mouse ficolin-A.
A;Reference number: JC5980; MUID:98205801; PMID:9535745
A;Accession: JC5980
A;Molecule type: mRNA
A;Residues: 1-334 <FUJ>
A;Cross-references: UNIPROT:O70165; DDBJ:AB007813; NID:G2957011; PIDN:BAA25126.1; PID:dl
C;Experimental source: liver
C;Comment: This protein consists of both collagen- and fibrinogen- like domains.
F;1-21/Domain: signal sequence #status predicted <SIG>
F;50-64,68-106/Domain: collagen-like #status predicted <COL>
F;123-334/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 40.8%; Score 60; DB 2; Length 334;
Best Local Similarity 60.0%; Pred. No. 4.6;
Matches 12; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 GMSGAGSGWEGSGSPPGV 20
| | | | | | | | | | | | | | | | | | | | | |
Db 77 GMSGAGSGKGEPGTMGPPGV 96

RESULT 2

CGB07S
collagen alpha 1(III) chain - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 09-Jul-2004
C;Accession: A02862; A38001; A38002; A38003; A38004; A38005; S71946
R;Fietzek, P.P.; Allmann, H.; Rauterberg, J.; Henkel, W.; Wachter, E.; Kuehn, K.
Hoppe-Seyler's Z. Physiol. Chem. 360, 809-820, 1979
A;Title: The covalent structure of calf skin type III collagen. I. The amino acid sequen
A;Reference number: A02862; MUID:80026026; PMID:488906
A;Accession: A02862
A;Molecule type: protein
A;Residues: 1-242 <FIE>
A;Cross-references: UNIPROT:P04258
R;Dewes, H.; Fietzek, P.P.; Kuehn, K.
Hoppe-Seyler's Z. Physiol. Chem. 360, 821-832, 1979
A;Title: The covalent structure of calf skin type III collagen. II. The amino acid seque
A;Reference number: A38001; MUID:80026027; PMID:488907
A;Accession: A38001
A;Molecule type: protein
A;Residues: 243-422 <DEW1>
R;Bentz, H.; Fietzek, P.P.; Kuehn, K.
Hoppe-Seyler's Z. Physiol. Chem. 360, 833-840, 1979

A;Reference number: I54365; MUID:95187161; PMID:7881420
A;Accession: I68663
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 663-675, 'V', 677, 'P', 679-742, 'A', 744-746 <FOR>
A;Cross-references: GB:L47668; NID:g1009095; PIDN:AAB59577.1; PID:g1009096
R;Niyibizi, C.; Bonadio, J.; Byers, P.H.; Eyre, D.R.
J. Biol. Chem. 267, 23108-23112, 1992
A;Title: Incorporation of type I collagen molecules that contain a mutant alpha 2(I) chain
A;Reference number: I55369; MUID:93054637; PMID:1385413
A;Accession: I55369
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 665-666, 'D', 668-670 <NIY>
A;Cross-references: GB:L00613; NID:g180888; PIDN:AAB59384.1; PID:g180889
A;Note: mutant sequence from a patient with osteogenesis imperfecta
R;Bateman, J.F.; Hannagan, M.; Chan, D.; Cole, W.G.
Biochem. J. 276, 765-770, 1991
A;Title: Characterization of a type I collagen alpha 2(I) glycine-586 to valine substitution
e method.
A;Reference number: A56799; MUID:91291136; PMID:2064612
A;Accession: A56799
A;Molecule type: mRNA
A;Residues: 672-675, 'V', 677, 'P', 679-681 <BAT>
A;Cross-references: GB:S39878; NID:g1679911; PIDN:AAB19314.1; PID:g232761
A;Note: sequence extracted from NCB1 backbone (NCBIN:39878, NCBIP:39886)
A;Note: mutant sequence of patient with osteogenesis imperfecta type IV; the authors suggest
ntrol sequence
R;Maeckelae, J.K.; Vuorio, T.; Vuorio, E.
Biochim. Biophys. Acta 1049, 171-176, 1990
A;Title: Growth-dependent modulation of type I collagen production and mRNA levels in cu
A;Reference number: S10768; MUID:90304220; PMID:2364107
A;Accession: S10768
A;Molecule type: mRNA
A;Residues: 960-1021, 'L', 1023-1188, 'D', 1190-1197, 'S', 1199-1356 <MAE>
A;Cross-references: EMBL:X55525; NID:g30101; PIDN:CAA39142.1; PID:g30102
A;Experimental source: fibroblast cell culture
R;Myers, J.C.; Chu, M.L.; Faro, S.H.; Clark, W.J.; Prockop, D.J.; Ramirez, F.
Proc. Natl. Acad. Sci. U.S.A. 78, 3516-3520, 1981
A;Title: Cloning a cDNA for the pro-alpha2 chain of human type I collagen.
A;Reference number: A18855; MUID:81273090; PMID:6267597
A;Accession: A18855
A;Molecule type: mRNA
A;Residues: 964-979, 'V', 981-1018, 'Q', 1020 <MYE>
A;Cross-references: GB:J00114; NID:g180393; PIDN:AAA51996.1; PID:g180394
A;Note: 1019-Leu was also found
R;Wenstrup, R.J.; Cohn, D.H.; Cohen, T.; Byers, P.H.
J. Biol. Chem. 263, 7734-7740, 1988
A;Title: Arginine for glycine substitution in the triple-helical domain of the products
A;Reference number: I55285; MUID:88227975; PMID:2897363
A;Accession: I55285
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1090-1107 <WEN1>
A;Cross-references: GB:M22816; NID:g179602; PIDN:AAA51844.1; PID:g179603
A;Accession: I70059
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1090-1101, 'R', 1103-1107 <WEN2>
A;Cross-references: GB:M22817; NID:g179606; PIDN:AAA51846.1; PID:g179607
A;Note: mutant sequence from a patient with osteogenesis imperfecta type IV
R;Myers, J.C.; Dickson, L.A.; de Wet, W.J.; Bernard, M.P.; Chu, M.L.; di Liberto, M.; Pe
J. Biol. Chem. 258, 10128-10135, 1983
A;Title: Analysis of the 3' end of the human pro-alpha-2(I) collagen gene. Utilization o
A;Reference number: S09175; MUID:83290853; PMID:6309769
A;Accession: S09175
A;Molecule type: DNA
Query Match 38.8%; Score 57; DB 1; Length 1366;
Best Local Similarity 47.6%; Pred. No. 46;
Matches 10; Conservative 1; Mismatches 10; Indels 0; Gaps 0;
QY 1 GMSGWEEGSGSPPGVT 21

Db 766 GPNPGPPGACSRGDDGGPPGMT 786
RESULT 11
JS0168
collagen col-8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C;Accession: JS0168
R;Cox, G.N.; Fields, C.; Kramer, J.M.; Rosenzweig, B.; Hirsh, D.
Gene 76, 331-344, 1989
A;Title: Sequence comparisons of developmentally regulated collagen genes of Caenorhabdi
A;Reference number: A91602; MUID:89326131; PMID:2753356
A;Accession: JS0168
A;Molecule type: DNA
A;Residues: 1-282 <COX>
A;Cross-references: UNIPROT:P18833; GB:M25479; NID:g156267; PIDN:AAA27993.1; PID:g156268
A;Note: the authors translated the codon ACG for residue 43 as Arg
C;Comment: col-8, col-7 and col-19 belong to the same group of collagen genes.
C;Genetics:
A;Gene: col-8
A;Map position: III
A;Introns: 133/1; 259/3
F;95-124/Domain: helical <HX1>
F;141-269/Domain: helical <HX2>
Query Match 38.1%; Score 56; DB 2; Length 282;
Best Local Similarity 47.6%; Pred. No. 12;
Matches 10; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
QY 1 GMSGWEEGSGSPPGVT 21
Db 150 GLVGPAGPAGDQGRHGPPGPT 170
RESULT 12
T16036
cuticle collagen col-8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T16036
R;Menezes, S.
submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid F11H8.
A;Reference number: Z18450
A;Accession: T16036
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-282 <MEN>
A;Cross-references: UNIPROT:P18833; EMBL:U40187; NID:g1055194; PID:g1055196; PIDN:AAA811
C;Genetics:
A;Gene: CESP:col-8
A;Introns: 133/1; 259/3
Query Match 38.1%; Score 56; DB 2; Length 282;
Best Local Similarity 47.6%; Pred. No. 12;
Matches 10; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
QY 1 GMSGWEEGSGSPPGVT 21
Db 150 GLVGPAGPAGDQGRHGPPGPT 170
RESULT 13
T18594
hypothetical protein AC3.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18594
R;McMurray, A.
submitted to the EMBL Data Library, April 1996
A;Reference number: Z18995

A;Accession: T18594
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-325 <WIL>
A;Cross-references: UNIPROT:Q17402; EMBL:Z711177; PIDN:CAA94869.1; GSPDB:GN00023; CESP:AC
A;Experimental source: clone AC3
C;Genetics:
A;Gene: CESP:AC3.6
A;Map position: 5
A;Introns: 47/3; 101/1; 270/3

Query Match 38.1%; Score 56; DB 2; Length 325;
Best Local Similarity 57.9%; Pred. No. 14;
Matches 11; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 GMOGPAGSGWEEGSGSPPG 19
DB 218 GSPGPAGSGRVRGGPPG 236

RESULT 14
B34493
collagen alpha 1(IX) chain long form precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 13-Jul-1990 #sequence revision 28-Oct-1994 #text_change 09-Jul-2004
C;Accession: B34493; S21861; A28360; B28360; S22243; A20982; A28754; A30973; S22240
R;Nishimura, I.; Muragaki, Y.; Olsen, B.R.
J. Biol. Chem. 264, 20033-20041, 1989
A;Title: Tissue-specific forms of type IX collagen-proteoglycan arise from the use of two
A;Reference number: A34493; MUID:90062114; PMID:2584206
A;Accession: B34493
A;Molecule type: mRNA
A;Residues: 1-416 <NIS>
A;Cross-references: UNIPROT:PI2106; UNIPROT:Q90779; GB:M28659; NID:g211623; PIDN:AAA4870
A;Note: the authors translated the codon TAC for residue 25 as Ile, GAA for residue 51 as
R;Olsen, B.R.
submitted to the EMBL Data Library, December 1987
A;Reference number: S21861
A;Accession: S21861
A;Molecule type: mRNA
A;Residues: 1-24,'I',26-50,'Q',52-299 <OLS>
A;Cross-references: EMBL:J03539; NID:g211573; PIDN:AAA48702.1; PID:g211574
R;Vasios, G.; Nishimura, I.; Konomi, H.; van der Rest, M.; Ninomiya, Y.; Olsen, B.R.
J. Biol. Chem. 263, 2324-2329, 1988
A;Title: Cartilage type IX collagen-proteoglycan contains a large amino-terminal globular
A;Reference number: A28360; MUID:88115376; PMID:3339014
A;Accession: A28360
A;Molecule type: mRNA
A;Residues: 1-24,'I',26-50,'Q',52-266 <VAS>
A;Cross-references: EMBL:J03539
A;Accession: B28360
A;Molecule type: protein
A;Residues: 31-38;49-50,'Q',52-54;97-114;152-158;259-266 <VA2>
R;Ninomiya, Y.; Castagnola, P.; Gerecke, D.; Gordon, M.K.; Jacenko, O.; LuValle, P.; McG
maguchi, N.; Olsen, B.R.
in Extracellular Matrix Genes, Sandell L.J. and Boyd C.D., eds., pp.79-114, Academic Pre
A;Title: The molecular biology of collagens with short triple-helical domains.
A;Reference number: S22243
A;Accession: S22243
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-24,'I',26-50,'Q',52-920 <NI1>
R;Ninomiya, Y.; Olsen, B.R.
Proc. Natl. Acad. Sci. U.S.A. 81, 3014-3018, 1984
A;Title: Synthesis and characterization of cDNA encoding a cartilage-specific short coll
A;Reference number: A20982; MUID:84221895; PMID:6328487
A;Accession: A20982
A;Molecule type: mRNA
A;Residues: 183-920 <NI2>
A;Cross-references: EMBL:X01702; NID:g211498; PIDN:AAA48675.1; PID:g211499
R;Lorano, G.; Ninomiya, Y.; Thompson, H.; Olsen, B.R.
Proc. Natl. Acad. Sci. U.S.A. 82, 4050-4054, 1985
A;Title: A distinct class of vertebrate collagen genes encodes chicken type IX collagen

A;Reference number: A94705; MUID:85216631; PMID:3858862
A;Accession: A28754
A;Molecule type: DNA
A;Residues: 833-920 <LOZ>
A;Cross-references: EMBL:M11324
R;van der Rest, M.; Mayne, R.; Ninomiya, Y.; Seidah, N.G.; Chretien, M.; Olsen, B.R.
J. Biol. Chem. 260, 220-225, 1985
A;Title: The structure of type IX collagen.
A;Reference number: A30973; MUID:85080081; PMID:2981204
A;Accession: A30973
A;Molecule type: protein
A;Residues: 262-272;778-782,'Q',784-797 <VAN>
R;Mayne, R.; van der Rest, M.; Ninomiya, Y.; Olsen, B.R.
Ann. N. Y. Acad. Sci. 460, 38-46, 1985
A;Title: The structure of type IX collagen.
A;Reference number: S22238; MUID:86185164; PMID:3868958
A;Accession: S22240
A;Molecule type: protein
A;Residues: 778-797 <MAY>
C;Genetics:
A;Introns: 5/2; 30/1; 56/1; 100/2; 232/3; 258/3; 265/3; 859/1
C;Keywords: alternative splicing; cartilage; coiled coil; extracellular matrix; glycopro
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-920/Product: collagen alpha 1(IX) chain #status predicted <MAT>
F;24-266/Domain: non-collagenous NC4 #status predicted <NC4>
F;267-403/Domain: collagenous COL3 #status predicted <COL3>
F;404-415/Domain: non-collagenous NC3 #status predicted <NC3>
F;416-754/Domain: collagenous COL2 #status predicted <COL2>
F;755-784/Domain: non-collagenous NC2 #status predicted <NC2>
F;785-899/Domain: collagenous COL1 #status predicted <COL1>
F;900-920/Domain: non-collagenous NC1 #status predicted <NC1>
F;44-198,242-252/Disulfide bonds: #status predicted
F;269,271,787,790,793,795/Modified site: hydroxyproline (Pro) #status experimental

Query Match 38.1%; Score 56; DB 2; Length 920;
Best Local Similarity 42.3%; Pred. No. 40;
Matches 11; Conservative 3; Mismatches 12; Indels 0; Gaps 0;

QY 1 GMOGPAGSGWEEGSGSPPGVTPLFSP 26
DB 617 GPRPPGSRGEPGPAGPGLPGKWWGP 642

RESULT 15
A43291
collagen alpha 2(I) chain precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A43291; A54328
R;Phillips, C.L.; Morgan, A.L.; Lever, L.W.; Wenstrup, R.J.
Genomics 13, 1345-1346, 1992
A;Title: Sequence analysis of a full-length cDNA for the murine pro alpha 2(I) collagen
A;Reference number: A43291; MUID:92372043; PMID:1505972
A;Accession: A43291
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-1373 <PHI>
A;Cross-references: UNIPROT:Q01149; GB:X58251; NID:g50488; PIDN:CAA41205.1; PID:g50489
A;Note: sequence extracted from NCBI backbone (NCBIP:112027)
R;Phillips, C.L.; Lever, L.W.; Pinnell, S.R.; Quarles, L.D.; Wenstrup, R.J.
J. Invest. Dermatol. 97, 980-984, 1991
A;Title: Construction of a full-length murine Proalpha2(I) collagen cDNA by the polymera
A;Reference number: A54328; MUID:92084969; PMID:1748823
A;Accession: A54328
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-110 <PH2>
C;Genetics:
A;Gene: COL1A2
C;Superfamily: collagen alpha 2(I) chain; fibrillar collagen carboxyl-terminal homology
C;Keywords: coiled coil; extracellular matrix; glycoprotein; trimer; triple helix
F;1145-1373/Domain: fibrillar collagen carboxyl-terminal homology <FCC>

Query Match 38.1%; Score 56; DB 1; Length 1373;
Best Local Similarity 48.0%; Pred. No. 61;
Matches 12; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 GMQGPAGSGWEEGSGSPPGVTPLFS 25
| | | | | : | | | | :
Db 60 GPPGPPGSPGPPGSPAPPGLTGNA 84

Search completed: October 29, 2005, 01:03:31
Job time : 17 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 29, 2005, 00:57:49 ; Search time 56 Seconds
(without alignments)
237.751 Million cell updates/sec

Title: US-09-980-263-1

Perfect score: 147

Sequence: 1 GMOGPAGSGWEEGSGPPGVTPLFSP 26

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	67	45.6	1378	2	O97405	O97405 haliotis di
2	67	45.6	1449	2	Q910C0	Q910C0 oncorhynchu
3	62	42.2	234	2	Q6BP25	Q6bp25 debaryomyce
4	62	42.2	640	2	Q6KAQ4	Q6kaq4 mus musculu
5	62	42.2	643	2	Q68ED0	Q68ed0 mus musculu
6	62	42.2	699	2	Q6P1C4	Q6pic4 mus musculu
7	62	42.2	1458	2	Q910B9	Q910b9 oncorhynchu
8	60	40.8	334	1	FCN1_MOUSE	O70165 mus musculu
9	60	40.8	1049	1	CA13_BOVIN	P04258 bos taurus
10	59.5	40.5	904	2	O76271	O76271 mytilus edu
11	59.5	40.5	905	2	Q8MW55	Q8mw55 mytilus gal
12	59	40.1	70	2	Q12985	Q12985 homo sapien
13	59	40.1	1447	2	Q6P4U1	Q6p4u1 brachydanio
14	59	40.1	1447	2	Q6U1J5	Q6ulj5 brachydanio
15	58.5	39.8	135	2	Q95LJ6	Q95lj6 macaca fasc
16	58.5	39.8	191	2	Q9CSM0	Q9csm0 mus musculu
17	58.5	39.8	386	2	Q01759	Q01759 pneumocysti
18	58.5	39.8	1076	2	Q01830	Q01830 pneumocysti
19	58.5	39.8	1077	2	Q6AHS1	Q6ahs1 pneumocysti
20	58	39.5	123	2	Q96ET3	Q96et3 homo sapien
21	58	39.5	164	2	Q7XDT8	Q7xdt8 oryza sativ
22	58	39.5	185	2	Q948R3	Q948r3 oryza sativ
23	58	39.5	185	2	Q7XDT6	Q7xdt6 oryza sativ
24	58	39.5	185	2	Q7XDT7	Q7xdt7 oryza sativ
25	58	39.5	251	2	Q96MW4	Q96mw4 homo sapien
26	58	39.5	313	2	Q96FI5	Q96fi5 homo sapien
27	58	39.5	322	2	Q9NSK5	Q9nsk5 caenorhabdi
28	58	39.5	393	2	Q7L8J4	Q7l8j4 homo sapien
29	58	39.5	421	2	Q9C0E3	Q9coe3 homo sapien
30	58	39.5	591	2	O82178	O82178 arabidopsis
31	58	39.5	703	1	CA28_HUMAN	P25067 homo sapien

32	58	39.5	888	2	Q90796	Q90796 gallus gall
33	58	39.5	998	2	Q8CFM4	Q8cfm4 mus musculu
34	58	39.5	1222	2	Q8K173	Q8k173 mus musculu
35	58	39.5	1464	1	CA13_MOUSE	P08121 mus musculu
36	58	39.5	1464	2	Q7TT32	Q7tt32 mus musculu
37	58	39.5	1464	2	Q8BK2	Q8bky2 mus musculu
38	58	39.5	1464	2	Q8BLW4	Q8bliw4 mus musculu
39	57.5	39.1	196	2	Q25947	Q25947 plasmodium
40	57.5	39.1	280	2	Q8BP14	Q8bpl4 mus musculu
41	57.5	39.1	280	2	Q8R138	Q8r138 mus musculu
42	57.5	39.1	2075	2	Q8JG44	Q8jg44 fugu rubrip
43	57.5	39.1	2075	2	Q90WA4	Q90wa4 fugu rubrip
44	57	38.8	317	1	YQ35_CAEEL	Q09456 caenorhabdi
45	57	38.8	618	2	Q9QXL4	Q9qxl4 rattus norv

ALIGNMENTS

RESULT 1						
O97405						
ID	O97405	PRELIMINARY;	PRT;	1378	AA.	
AC	O97405;					
DT	01-MAY-1999	(TrEMBLrel. 10, Created)				
DT	01-MAY-1999	(TrEMBLrel. 10, Last sequence update)				
DT	01-MAR-2004	(TrEMBLrel. 26, Last annotation update)				
DE	Collagen pro alpha-chain precursor.					
GN	Name=Hdcol 1 alpha;					
OS	Haliotis discus (Abalone).					
OC	Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;					
OC	Vetigastropoda; Haliotoidea; Haliotidae; Haliotis.					
OX	NCBI_TaxID=36094;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	TISSUE=Muscle;					
RX	MEDLINE=99234051; PubMed=10215888;					
RA	Yoneda C., Hirayama Y., Nakaya M., Matsubara Y., Irie S.,					
RA	Watabe S.;					
RT	"The occurrence of two types of collagen proalpha-chain in					
RT	Haliotis discus muscle.";					
RL	Eur. J. Biochem. 261:714-721(1999).					

Query Match						
Best Local Similarity 45.6%; Score 67; DB 2; Length 1378;						
Matches 12; Conservative 3; Mismatches 11; Indels 0; Gaps 0;						
QY	1 GMOGPAGSGWEEGSGSGPPGVTPLFSP 26					
	:					
Db	1111 GLTGACPSGPPGPPGPGYGVYSP 1136					

RESULT 2						
Q910C0						
ID	Q910C0	PRELIMINARY;	PRT;	1449	AA.	
AC	Q910C0;					
DT	01-DEC-2001	(TrEMBLrel. 19, Created)				
DT	01-DEC-2001	(TrEMBLrel. 19, Last sequence update)				

```
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Collagen a1(I).
GN Name=COL1A1;
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21257802; PubMed=11358497;
RA Saito M., Takenouchi Y., Kunisaki N., Kimura S.;
RT "Complete primary structure of rainbow trout type I collagen
  consisting of al(I)2(I)3(I) heterotrimers.";
RL Eur. J. Biochem. 268:2817-2827(2001).
DR EMBL; AB052835; BAB55661.1; -
DR GO; GO:0005581; C:collagen; IEA.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
DR GO; GO:0006817; P:phosphate transport; IEA.
DR Pfam; PF01410; COLFI; 1.
DR Pfam; PF01391; Collagen; 18.
DR Pfam; PF00093; VWC; 1.
DR ProDom; PD000007; Clg_helix; 4.
DR ProDom; PD002078; Fib_collagen_C; 1.
DR SMART; SM00038; COLFI; 1.
DR SMART; SM00214; VWC; 1.
DR PROSITE; PS01208; VWFC_1; 1.
DR PROSITE; PS50184; VWFC_2; 1.
KW Collagen.
SQ SEQUENCE 1449 AA; 137116 MW; 62EEF8A7BFD652B8 CRC64;

Query Match 45.6%; Score 67; DB 2; Length 1449;
Best Local Similarity 46.2%; Pred. No. 27;
Matches 12; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 GMOGPAGSGWEEGSGSPPGVTPFLFSP 26
|:|:|:|:|:|:|:|:|:|
Db 608 GVAGPSGERGEQGAGGPPGFQGLSGP 633

RESULT 3
Q6BP25 PRELIMINARY; PRT; 234 AA.
AC Q6BP25;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Similarity.
GN ORFNames=DEHA0E17853g;
OS Debaryomyces hansenii CBS767.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Debaryomycetes.
OX NCBI_TaxID=284592;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CBS767;
RG Genolevures;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talia E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Bolaram A., Boyer E., Cattolico L., Confanioleri F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Swennene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zenlou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Wincker P., Souciet J.L.;
RT "Genome evolution in yeasts."

RL Nature 430:35-44(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CBS767;
RA Genoscope;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR382137; CAG88303.1; -
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0006817; P:phosphate transport; IEA.
DR InterPro; IPR008161; Clg_helix.
DR InterPro; IPR008160; Collagen.
DR Pfam; PF01391; Collagen; 3.
DR ProDom; PD000007; Clg_helix; 1.
KW Collagen.
SQ SEQUENCE 234 AA; 22636 MW; 3C0B851B5D0095C9 CRC64;

Query Match 42.2%; Score 62; DB 2; Length 234;
Best Local Similarity 60.0%; Pred. No. 16;
Matches 12; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 GMOGPAGSGWEEGSGSPPGV 20
|:|:|:|:|:|:|:|:|:|
Db 126 GDQGPXGAGGIRGIGPGQGV 145

RESULT 4
Q6KAQ4 PRELIMINARY; PRT; 640 AA.
AC Q6KAQ4;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE MFLJ00201 protein (Fragment).
GN Name=MFLJ00201;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryonic tail;
RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
RA Saga Y., Kitamura H., Nakagawa T., Nagase T., Ohara O., Koga H.;
RT "Prediction of the Coding Sequences of Mouse Homologues of FLJ Genes:
  The Complete Nucleotide Sequences of 110 Mouse FLJ-Homologous cDNAs
  Identified by Screening of Terminal Sequences of cDNA Clones Randomly
  Sampled from Size-Fractionated Libraries.";
RL DNA Res. 11:167-180(2004).
DR EMBL; AK131153; BAD21403.1; -
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0006817; P:phosphate transport; IEA.
DR InterPro; IPR001073; Clq.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR008983; TNF_like.
DR Pfam; PF00386; Clq; 1.
DR Pfam; PF01391; Collagen; 8.
DR PRINTS; PR00007; COMPLEMTCLQ.
DR SMART; SM00110; Clq; 1.
DR PROSITE; PS01113; Clq; 1.
KW Collagen.
FT NON TER
SQ SEQUENCE 640 AA; 61034 MW; 75CC9DEBAE5AC4B5 CRC64;

Query Match 42.2%; Score 62; DB 2; Length 640;
Best Local Similarity 60.0%; Pred. No. 45;
Matches 12; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 GMOGPAGSGWEEGSGSPPGV 20
|:|:|:|:|:|:|:|:|:|
Db 307 GRRGPPGSKGEVGPVGGPPGV 326

RESULT 5
```

Q68ED0 Q68ED0 PRELIMINARY; PRT; 643 AA.

AC Q68ED0;

DT 25-OCT-2004 (TrEMBLrel. 28, Created)

DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)

DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)

DE Col8a2 protein.

GN Name=Col8a2;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6; TISSUE=Brain;

RX PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Touchman J.W., Green E.D., Dickson M.C., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6; TISSUE=Brain;

RA Strausberg R.;

RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC080317; AAH80317.1; -.

DR InterPro; IPR001073; Clq.

DR InterPro; IPR008160; Collagen.

DR InterPro; IPR008983; TNF_like.

DR Pfam; PF00386; Clq; 1.

DR Pfam; PF01391; Collagen; 8.

DR PRINTS; PR00007; COMPLEMENTC1Q.

DR SMART; SM00110; Clq; 1.

DR PROSITE; PS01113; Clq; 1.

SQ SEQUENCE .643 AA; 61831 MW; FE19B6CE5AAB2A8B CRC64;

Query Match 42.2%; Score 62; DB 2; Length 643;

Best Local Similarity 60.0%; Pred. No. 46;

Matches 12; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GMOGPAGSGWEEGSGSPPGV 20

Db 310 GRRGPPGSGEVGPGPGPV 329

RESULT 6

Q6P1C4

ID Q6P1C4 PRELIMINARY; PRT; 699 AA.

AC Q6P1C4;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Procollagen, type VIII, alpha 2.

GN Name=Col8a2;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6; TISSUE=Brain;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Touchman J.W., Green E.D., Dickson M.C., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6; TISSUE=Brain;

RA Strausberg R.;

RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC065148; AAH65148.1; -.

DR GO; GO:0005737; C:cytoplasm; IEA.

DR GO; GO:0006817; P:phosphate transport; IEA.

DR InterPro; IPR001073; Clq.

DR InterPro; IPR008160; Collagen.

DR InterPro; IPR008983; TNF_like.

DR Pfam; PF00386; Clq; 1.

DR Pfam; PF01391; Collagen; 8.

DR PRINTS; PR00007; COMPLEMENTC1Q.

DR SMART; SM00110; Clq; 1.

DR PROSITE; PS01113; Clq; 1.

KW Collagen.

SQ SEQUENCE .699 AA; 66943 MW; FCBD4FBB44642646 CRC64;

Query Match 42.2%; Score 62; DB 2; Length 699;

Best Local Similarity 60.0%; Pred. No. 50;

Matches 12; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GMOGPAGSGWEEGSGSPPGV 20

Db 366 GRRGPPGSGEVGPGPGPV 385

RESULT 7

Q910B9

ID Q910B9 PRELIMINARY; PRT; 1458 AA.

AC Q910B9;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Collagen a3(I).

GN Name=COL1A3;

OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;

OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

OX NCBI_TaxID=8022;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21257802; PubMed=11358497;

RA Saito M., Takenouchi Y., Kunisaki N., Kimura S.;

RT "Complete primary structure of rainbow trout type I collagen consisting of a1(I)a2(I)a3(I) heterotrimers.";

```

RL Eur. J. Biochem. 268:2817-2827(2001).
DR EMBL; AB052836; BAB55662.1; -.
DR GO; GO:0005581; C:collagen; IEA.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
DR GO; GO:0006817; P:phosphate transport; IEA.
DR Pfam; PF01410; COLFI; 1.
DR Pfam; PF01391; Collagen; 18.
DR ProDom; PD000007; Clg_helix; 2.
DR ProDom; PD002078; Fib_collagen_C; 1.
DR SMART; SM00038; COLFI; 1.
DR SMART; SM00214; VWC; 1.
DR PROSITE; PS01208; VWFC_1; 1.
DR PROSITE; PS50184; VWFC_2; 1.
KW Collagen.
SQ SEQUENCE 1458 AA; 137757 MW; AB1F9F3410A98650 CRC64;

Query Match 42.2%; Score 62; DB 2; Length 1458;
Best Local Similarity 63.2%; Pred. No. 1.1e+02;
Matches 12; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 GMQGPAGSGWEEGSGSPPG 19
DB 611 GPQGPAGSQGKEGEGPAG 629

RESULT 8
FCN1 MOUSE STANDARD; PRT; 334 AA.
ID FCN1 MOUSE
AC O70165;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ficolin 1 precursor (Collagen/fibrinogen domain-containing protein 1)
DE (Ficolin-A) (Ficolin A) (M-Ficolin).
GN Name=Fcn1; Synonyms=Fcna;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Liver;
RX MEDLINE=98205801; PubMed=9535745; DOI=10.1006/bbrc.1998.8344;
RA Fujimori Y., Harumiya S., Fukumoto Y., Miura Y., Yagasaki K.,
RA Tachikawa H., Fujimoto D.;
RT "Molecular cloning and characterization of mouse ficolin-A.";
RL Biochem. Biophys. Res. Commun. 244:796-800(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Involved in serum exerting lectin activity. Binds GlcNAc
(CC (By similarity)).

-!- SUBUNIT: Homopolymer. Interacts with elastin (By similarity).
-!- SUBCELLULAR LOCATION: Secreted. Found on the monocyte surface (By
similarity).
-!- TISSUE SPECIFICITY: Highly expressed in liver and spleen.
-!- SIMILARITY: Belongs to the ficolin lectin family.
-!- SIMILARITY: Contains 1 collagenous domain.
-!- SIMILARITY: Contains 1 fibrinogen C-terminal domain.
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or send an email to license@isb-sib.ch).
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EMBL; AB007813; BAA25126.1; -.
DR EMBL; BC019180; AAH19180.1; -.
DR PIR; JC5980; JC5980.
DR HSSP; P02671; 1FZD.
DR MGD; MGI:1340905; Fcna.
DR InterPro; IPR008161; Clg_helix.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF01391; Collagen; 1.
DR Pfam; PF00147; Fibrinogen_C; 1.
DR ProDom; PD000007; Clg_helix; 1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
DR Collagen; Glycoprotein; Lectin; Multigene family; Repeat; Signal.
KW CHAIN 1 22 Potential.
FT SIGNAL 1 22 Ficolin 1.
FT CHAIN 23 334 Collagen-like.
FT DOMAIN 50 88 Fibrinogen C-terminal.
FT DOMAIN 152 298 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 261 261
SQ SEQUENCE 334 AA; 36298 MW; 9D30C05036AA04B1 CRC64;

Query Match 40.8%; Score 60; DB 1; Length 334;
Best Local Similarity 60.0%; Pred. No. 40;
Matches 12; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 GMQGPAGSGWEEGSGSPPGV 20
DB 77 GKMGPAKSGKEPGTGMPPGV 96

RESULT 9
CAL3 BOVIN STANDARD; PRT; 1049 AA.
ID CAL3 BOVIN
AC P04258;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Collagen alpha 1(III) chain.
GN Name=COL3A1;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE OF 1-242.
RX MEDLINE=80026026; PubMed=488906;
RA Fietzek P.P., Allmann H., Rauterberg J., Henkel W., Wachter E.,
RA Kuhn K.;
RT "The covalent structure of calf skin type III collagen. I. The amino
RT acid sequence of the amino terminal region of the alpha 1(III) chain
RT (positions 1-222).";
RL Hoppe-Seyler's Z. Physiol. Chem. 360:809-820(1979).
RN [2]
RP SEQUENCE OF 243-422.
RX MEDLINE=80026027; PubMed=488907;
RA Dewes H., Fietzek P.P., Kuhn K.;
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QY      1 GMOGPAGSGWEEGSGSPPGVTPLEFSP 26
Db      232 GPRGPAGPPGDQGHGGPPG-PPGHSP 256

RESULT 12
Q12985
ID      Q12985      PRELIMINARY;      PRT;      70 AA.
AC      Q12985;
DT      01-NOV-1996 (TrEMBLrel. 01, Created)
DT      01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT      01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE      Alpha-1 type II collagen (Fragment).
GN      Name=COL2A1;
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Blood;
RX      MEDLINE=95150028; PubMed=7847372;
RA      Tiller G.E., Weis M.A., Polumbo P.A., Gruber H.E., Rimoin D.L.,
RA      Cohn D.H., Eyre D.R.;
RT      "An RNA-splicing mutation (G+51VS20) in the type II collagen gene
RT      (COL2A1) in a family with spondyloepiphyseal dysplasia congenita.";
RL      Am. J. Hum. Genet. 56:388-395(1995).
DR      EMBL; U15195; AAB60370.1; -.
DR      PIR; A38513; CGHU6C.
DR      GO; GO:0005737; C:cytoplasm; IEA.
DR      GO; GO:0006817; P:phosphate transport; IEA.
DR      InterPro; IPR008161; Clg_helix.
DR      InterPro; IPR008160; Collagen.
DR      Pfam; PF01391; Collagen; 1.
DR      ProDom; PD000007; Clg_helix; 1.
DR      Collagen.
KW      NON_TER      1
FT      NON_TER      70
SQ      SEQUENCE      70 AA; 6482 MW; 13AE3044C3F2FC07 CRC64;

Query Match      40.1%; Score 59; DB 2; Length 70;
Best Local Similarity      46.7%; Pred. No. 11;
Matches      14; Conservative      1; Mismatches      11; Indels      4; Gaps      1;

QY      1 GMOGPAGSGWEEGS----GSPPGVTPLEFSP 26
Db      38 GPQGPAGPEEGKRGARGEPGGVGPIGPP 67

RESULT 13
Q6P4U1
ID      Q6P4U1      PRELIMINARY;      PRT;      1447 AA.
AC      Q6P4U1;
DT      05-JUL-2004 (TrEMBLrel. 27, Created)
DT      05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT      05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE      Collal protein.
GN      Name=collal;
OS      Brachydanio rerio (Zebrafish) (Danio rerio).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC      Cyprinidae; Danio.
OX      NCBI_TaxID=7955;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Embryo;
RX      MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA      Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA      Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA      Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA      Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA      Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
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RA      Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA      Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA      Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA      Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA      Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA      Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA      Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA      Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA      Jones S.J., Marra M.A.;
RT      "Generation and initial analysis of more than 15,000 full-length human
RT      and mouse cDNA sequences.";
RL      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Embryo;
RA      Strausberg R.;
RL      Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR      EMBL; BC063249; AAH63249.1; -.
DR      ZFIN; ZDB-GENE-030131-9102; colla1.
DR      GO; GO:0005581; C:collagen; IEA.
DR      GO; GO:0005737; C:cytoplasm; IEA.
DR      GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
DR      GO; GO:0006817; P:phosphate transport; IEA.
DR      InterPro; IPR008161; Clg_helix.
DR      InterPro; IPR008160; Collagen.
DR      InterPro; IPR000885; Fib_collagen_C.
DR      InterPro; IPR009041; PMP_SGCI.
DR      InterPro; IPR001007; VWF_C.
DR      Pfam; PF01410; COLFI; 1.
DR      Pfam; PF01391; Collagen; 17.
DR      Pfam; PF00093; VWC; 1.
DR      ProDom; PD000007; Clg_helix; 1.
DR      ProDom; PD002078; Fib_collagen_C; 1.
DR      SMART; SM00038; COLFI; 1.
DR      SMART; SM00214; VWC; 1.
DR      PROSITE; PS01208; VWFC_1; 1.
DR      PROSITE; PS50184; VWFC_2; 1.
KW      Collagen.
SQ      SEQUENCE      1447 AA; 136955 MW; 74723FC8ACAAAD86 CRC64;

Query Match      40.1%; Score 59; DB 2; Length 1447;
Best Local Similarity      46.2%; Pred. No. 2.4e+02;
Matches      12; Conservative      2; Mismatches      12; Indels      0; Gaps      0;

QY      1 GMOGPAGSGWEEGSGSPPGVTPLEFSP 26
Db      607 GPAGPAGERGEQGAAGPPGFQGLPGP 632

RESULT 14
Q6U1J5
ID      Q6U1J5      PRELIMINARY;      PRT;      1447 AA.
AC      Q6U1J5;
DT      05-JUL-2004 (TrEMBLrel. 27, Created)
DT      05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT      05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE      Chihuahua.
GN      Name=collal; Synonyms=chi;
OS      Brachydanio rerio (Zebrafish) (Danio rerio).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC      Cyprinidae; Danio.
OX      NCBI_TaxID=7955;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=22984997; PubMed=14623232; DOI=10.1016/S0012-1606(03)00399-3;
RA      Fisher S., Jagadeeswaran P., Halpern M.E.;
RT      "Radiographic analysis of zebrafish skeletal defects.";
RL      Dev. Biol. 264:64-76(2003).
DR      EMBL; AY380817; AAR24536.1; -.
DR      ZFIN; ZDB-GENE-030131-9102; colla1.
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DR GO; GO:0005581; C:collagen; IEA.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
DR GO; GO:0006817; P:phosphate transport; IEA.

DR InterPro; IPR008160; Collagen.
DR InterPro; IPR000885; Fib_collagen_C.
DR InterPro; IPR009041; PMP_SGCI.
DR InterPro; IPR001007; VWF_C.

DR Pfam; PF01410; COLFI; 1.
DR Pfam; PF01391; Collagen; 16.
DR Pfam; PF00093; VWC; 1.
DR ProDom; PD002078; Fib_collagen_C; 1.

DR SMART; SM00038; COLFI; 1.
DR SMART; SM00214; VWC; 1.
DR PROSITE; PS01208; VWFC_1; 1.
DR PROSITE; PS50184; VWFC_2; 1.

KW Collagen.
SQ SEQUENCE 1447 AA; 137144 MW; 9CABD561F5BA36BF CRC64;

Query Match 40.1%; Score 59; DB 2; Length 1447;
Best Local Similarity 46.2%; Pred. No. 2.4e+02;
Matches 12; Conservative 2; Mismatches 12; Indels 0; Gaps 0;

QY 1 GMSGPAGSGWEEGSGSPPGVTPLFSP 26
| | | | | : | : | | | | |
Db 607 GPAGPAGERGEQGAAGPPGFQGLPGP 632

RESULT 15

Q95LJ6 PRELIMINARY; PRT; 135 AA.

AC Q95LJ6;
.DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.

RC TISSUE=Testis;
RA Osada N., Hida M., Kusuda J., Tanuma R., Hirata M., Suto Y., Hirai M.,
RA Terao K., Sugano S., Hashimoto K.;
RT "Cynomolgus monkey testicular cDNAs for discovery of novel human genes
RT in the human genome sequence.";
RL BMC Genomics 3:36-36(2002).
DR EMBL; AB072792; BAB69761.1; -.
KW Hypothetical protein.
SQ SEQUENCE 135 AA; 14280 MW; 398CC2768FFFA25D7 CRC64;

Query Match 39.8%; Score 58.5; DB 2; Length 135;
Best Local Similarity 45.5%; Pred. No. 24;
Matches 15; Conservative 1; Mismatches 8; Indels 9; Gaps 2;

QY 3 QGPAG-SWEEGSGSP-----PGVTPLFSP 26
: | | | | | | | | | | | | | | |
Db 82 RGPVGASGWAGCASPQTSLTPYPRVTPCQVP 114

Search completed: October 29, 2005, 01:04:35
Job time : 60 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 29, 2005, 01:01:09 ; Search time 41 Seconds
(without alignments)
47.338 Million cell updates/sec

Title: US-09-980-263-1
Perfect score: 147
Sequence: 1 GMOGPAGSGWEEGSGPPGVTPPLFSP 26

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	147	100.0	26	2	US-08-370-156-27
2	147	100.0	31	2	US-08-370-156-11
3	147	100.0	31	3	US-08-990-065-23
4	147	100.0	31	3	US-08-975-084-3
5	147	100.0	31	4	US-09-380-532-13
6	147	100.0	600	2	US-08-370-156-4
7	147	100.0	600	3	US-08-814-095-4
8	147	100.0	600	3	US-08-975-084-1
9	140	95.2	25	3	US-08-975-084-2
10	60	40.8	54	1	US-07-972-032-59
11	60	40.8	54	1	US-08-642-255-71
12	60	40.8	93	1	US-07-972-032-60
13	60	40.8	93	1	US-07-972-032-61
14	60	40.8	633	1	US-08-642-255-73
15	60	40.8	1065	1	US-08-642-255-72
16	59	40.1	532	1	US-08-494-168-9
17	57.5	39.1	280	3	US-09-383-586-18
18	57.5	39.1	280	4	US-09-823-038A-18
19	57	38.8	520	4	US-09-252-991A-29451
20	57	38.8	1024	3	US-08-931-820-2
21	57	38.8	1366	3	US-08-963-825-19
22	57	38.8	1366	3	US-09-500-811-19
23	57	38.8	1366	3	US-09-570-573-19
24	57	38.8	1366	3	US-09-548-608-19
25	57	38.8	1366	4	US-09-585-887-10
26	57	38.8	1366	4	US-09-289-578-10
27	57	38.8	1366	4	US-09-949-016-5882

28	57	38.8	1442	2	US-08-316-650-12	Sequence 12, Appl
29	57	38.8	1442	5	PCT-US95-02251-12	Sequence 12, Appl
30	56	38.1	161	4	US-09-252-991A-17843	Sequence 17843, A
31	56	38.1	475	4	US-09-252-991A-26219	Sequence 26219, A
32	55.5	37.8	549	1	US-08-494-168-8	Sequence 8, Appli
33	55.5	37.8	1712	4	US-09-961-403-9	Sequence 9, Appli
34	55	37.4	101	3	US-08-990-571-68	Sequence 68, Appl
35	55	37.4	101	4	US-09-528-784A-68	Sequence 68, Appl
36	55	37.4	101	4	US-09-569-098A-68	Sequence 68, Appl
37	55	37.4	105	3	US-08-990-571-69	Sequence 69, Appl
38	55	37.4	105	4	US-09-528-784A-69	Sequence 69, Appl
39	55	37.4	105	4	US-09-569-098A-69	Sequence 69, Appl
40	55	37.4	504	4	US-09-252-991A-20694	Sequence 20694, A
41	55	37.4	1057	3	US-08-931-820-4	Sequence 4, Appli
42	55	37.4	1739	4	US-09-795-061-2	Sequence 2, Appli
43	54	36.7	18	1	US-07-972-032-84	Sequence 84, Appl
44	54	36.7	18	1	US-08-642-255-135	Sequence 135, App
45	54	36.7	30	3	US-08-845-258-47	Sequence 47, Appl

ALIGNMENTS

RESULT 1
US-08-370-156-27
; Sequence 27, Application US/08370156
; Patent No. 5932780
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Shani, Moshe
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
; TITLE OF INVENTION: ANTICHOLINESTERASE SUBSTANCES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reising, Ethington, Barnard & Perry
; STREET: P.O. Box 4390
; CITY: Troy
; STATE: Michigan
; COUNTRY: US
; ZIP: 48099
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/370,156
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: P-307 (Mulford)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810) 689-3500
; TELEFAX: (810) 689-4071
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-370-156-27

Query Match 100.0%; Score 147; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 7.7e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GMOGPAGSGWEEGSGPPGVTPPLFSP 26
|||
Db 1 GMOGPAGSGWEEGSGPPGVTPPLFSP 26

RESULT 2
 US-08-370-156-11
 ; Sequence 11, Application US/08370156
 ; Patent No. 5932780
 ; GENERAL INFORMATION:
 ; APPLICANT: Soreq, Hermona
 ; APPLICANT: Zakut, Haim
 ; APPLICANT: Shani, Moshe
 ; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
 ; TITLE OF INVENTION: ANTICHOLINESTERASE SUBSTANCES
 ; NUMBER OF SEQUENCES: 27
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Reising, Ethington, Barnard & Perry
 ; STREET: P.O. Box 4390
 ; CITY: Troy
 ; STATE: Michigan
 ; COUNTRY: US
 ; ZIP: 48099
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/370,156
 ; FILING DATE:
 ; CLASSIFICATION: 536
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kohn, Kenneth I.
 ; REGISTRATION NUMBER: 30,955
 ; REFERENCE/DOCKET NUMBER: P-307 (Mulford)
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (810) 689-3500
 ; TELEFAX: (810) 689-4071
 ; INFORMATION FOR SEQ ID NO: 11:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 31 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-370-156-11

Query Match 100.0%; Score 147; DB 2; Length 31;
 Best Local Similarity 100.0%; Pred. No. 9.2e-11;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GMOGPAGSGWEEGSGSPPGVTPLFSP 26
 Db 6 GMOGPAGSGWEEGSGSPPGVTPLFSP 31
 RESULT 3
 US-08-990-065-23
 ; Sequence 23, Application US/08990065
 ; Patent No. 6121046
 ; GENERAL INFORMATION:
 ; APPLICANT: Soreq, Hermona
 ; APPLICANT: Seidman, Shlomo
 ; APPLICANT: Eckstein, Fritz
 ; APPLICANT: Friedman, Alon
 ; APPLICANT: Kaufman, Daniela
 ; TITLE OF INVENTION: SYNTHETIC ANTISENSE
 ; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDES AND PHARMACEUTICAL COMPOSITIONS
 ; NUMBER OF SEQUENCES: 23
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Kohn & Associates
 ; STREET: 30500 No. 6121046thwestern Hwy. Suite 410
 ; CITY: Farmington Hills
 ; STATE: Michigan
 ; COUNTRY: U.S.
 ; ZIP: 48334

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/990,065
 FILING DATE:
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/850,347
 FILING DATE: 02-MAY-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/318,826
 FILING DATE: 01-JAN-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Montgomery, Ilene N.
 REGISTRATION NUMBER: 38,972
 REFERENCE/DOCKET NUMBER: 2391.00086
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (248) 539-5050
 TELEFAX: (248) 539-5055
 INFORMATION FOR SEQ ID NO: 23:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 31 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-990-065-23
 Query Match 100.0%; Score 147; DB 3; Length 31;
 Best Local Similarity 100.0%; Pred. No. 9.2e-11;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GMOGPAGSGWEEGSGSPPGVTPLFSP 26
 Db 6 GMOGPAGSGWEEGSGSPPGVTPLFSP 31
 RESULT 4
 US-08-975-084-3
 ; Sequence 3, Application US/08975084
 ; Patent No. 6258780
 ; GENERAL INFORMATION:
 ; APPLICANT: Soreq, Hermona
 ; APPLICANT: FRIEDMAN, Alon
 ; APPLICANT: SEIDMAN, Shlomo
 ; APPLICANT: KAUFER, Daniela
 ; TITLE OF INVENTION: A METHOD AND COMPOSITION FOR ENABLING
 ; TITLE OF INVENTION: PASSAGE THROUGH THE BLOOD-BRAIN-BARRIER
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Kohn & Associates
 ; STREET: 30500 No. 6258780thwestern Hwy., Suite 410
 ; CITY: Farmington Hills
 ; STATE: Michigan
 ; COUNTRY: US
 ; ZIP: 48334
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/975,084
 ; FILING DATE: 11-NOV-1997
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Montgomery, Ilene N.
 ; REGISTRATION NUMBER: 38,972
 ; REFERENCE/DOCKET NUMBER: 2391.00082
 ; TELECOMMUNICATION INFORMATION:

```

; TELEPHONE: (248) 539-5050
; TELEFAX: (248) 539-5055
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-975-084-3

Query Match 100.0%; Score 147; DB 3; Length 31;
Best Local Similarity 100.0%; Pred. No. 9.2e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GMOGPAGSGWEEGSGSPPGVTPLFSP 26
Db 6 GMOGPAGSGWEEGSGSPPGVTPLFSP 31

RESULT 5
US-09-380-532-13
; Sequence 13, Application US/09380532
; Patent No. 6475998
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; Seidman, Shlomo
; Shohami, Esther
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; TREATMENT OF INJURY TO THE CENTRAL NERVOUS SYSTEM
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kohn & Associates
; STREET: 30500 No. 6475998thwestern Hwy.
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: US
; ZIP: 48334
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/380,532
; FILING DATE: 12-No. 6475998-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Montgomery, Ilene N.
; REGISTRATION NUMBER: 38,972
; REFERENCE/DOCKET NUMBER: 2391.00089
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (248) 539-5050
; TELEFAX: (248) 539-5055
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-380-532-13

Query Match 100.0%; Score 147; DB 4; Length 31;
Best Local Similarity 100.0%; Pred. No. 9.2e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GMOGPAGSGWEEGSGSPPGVTPLFSP 26
Db 6 GMOGPAGSGWEEGSGSPPGVTPLFSP 31

US-08-975-084-3
; TELEPHONE: (248) 539-5050
; TELEFAX: (248) 539-5055
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-975-084-3

Query Match 100.0%; Score 147; DB 3; Length 31;
Best Local Similarity 100.0%; Pred. No. 9.2e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GMOGPAGSGWEEGSGSPPGVTPLFSP 26
Db 6 GMOGPAGSGWEEGSGSPPGVTPLFSP 31

RESULT 6
US-08-370-156-4
; Sequence 4, Application US/08370156
; Patent No. 5932780
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Shani, Moshe
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
; TITLE OF INVENTION: ANTICHOLINESTERASE SUBSTANCES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reising, Ethington, Barnard & Perry
; STREET: P.O. Box 4390
; CITY: Troy
; STATE: Michigan
; COUNTRY: US
; ZIP: 48099
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/370,156
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: P-307 (Mulford)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810) 689-3500
; TELEFAX: (810) 689-4071
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 600 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-370-156-4

Query Match 100.0%; Score 147; DB 2; Length 600;
Best Local Similarity 100.0%; Pred. No. 1.8e-09;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GMOGPAGSGWEEGSGSPPGVTPLFSP 26
Db 575 GMOGPAGSGWEEGSGSPPGVTPLFSP 600

RESULT 7
US-08-814-095-4
; Sequence 4, Application US/08814095
; Patent No. 6025183
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Shani, Moshe
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
; TITLE OF INVENTION: ANTI-CHOLINESTERASE SUBSTANCES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KOHN & ASSOCIATES
; STREET: 30500 No. 6025183thwestern Highway, Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: U.S.
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QY 1 GMOGPAGSGWEEGSGSPPGVTPLFSP 26
Db 6 GMOGPAGSGWEEGSGSPPGVTPLFSP 31

RESULT 6
US-08-370-156-4
; Sequence 4, Application US/08370156
; Patent No. 5932780
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Shani, Moshe
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
; TITLE OF INVENTION: ANTICHOLINESTERASE SUBSTANCES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reising, Ethington, Barnard & Perry
; STREET: P.O. Box 4390
; CITY: Troy
; STATE: Michigan
; COUNTRY: US
; ZIP: 48099
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/370,156
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: P-307 (Mulford)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810) 689-3500
; TELEFAX: (810) 689-4071
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 600 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-370-156-4

Query Match 100.0%; Score 147; DB 2; Length 600;
Best Local Similarity 100.0%; Pred. No. 1.8e-09;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GMOGPAGSGWEEGSGSPPGVTPLFSP 26
Db 575 GMOGPAGSGWEEGSGSPPGVTPLFSP 600

RESULT 7
US-08-814-095-4
; Sequence 4, Application US/08814095
; Patent No. 6025183
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Shani, Moshe
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
; TITLE OF INVENTION: ANTI-CHOLINESTERASE SUBSTANCES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KOHN & ASSOCIATES
; STREET: 30500 No. 6025183thwestern Highway, Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: U.S.
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; ZIP: 48334
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/814,095
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Montgomery, Ilene N.
; REGISTRATION NUMBER: 38,972
; REFERENCE/DOCKET NUMBER: 2391.00066
; TELEPHONE: (248) 539-5050
; TELEFAX: (248) 539-5055
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 600 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-814-095-4

Query Match 100.0%; Score 147; DB 3; Length 600;
Best Local Similarity 100.0%; Pred. No. 1.8e-09;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GMOGPAGSGWEEGSGSPPGVTPLFSP 26
Db 575 GMOGPAGSGWEEGSGSPPGVTPLFSP 600

RESULT 8
US-08-975-084-1
; Sequence 1, Application US/08975084
; Patent No. 6258780
; GENERAL INFORMATION:
; APPLICANT: SOREQ, Hermona
; APPLICANT: FRIEDMAN, Alon
; APPLICANT: SEIDMAN, Shlomo
; APPLICANT: KAUFER, Daniela
; TITLE OF INVENTION: A METHOD AND COMPOSITION FOR ENABLING
; TITLE OF INVENTION: PASSAGE THROUGH THE BLOOD-BRAIN-BARRIER
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kohn & Associates
; STREET: 30500 No. 6258780thwestern Hwy., Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: US
; ZIP: 48334
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,084
; FILING DATE: 11-NOV-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Montgomery, Ilene N.
; REGISTRATION NUMBER: 38,972
; REFERENCE/DOCKET NUMBER: 2391.00082
; TELEPHONE: (248) 539-5050
; TELEFAX: (248) 539-5055
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 600 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-814-095-4
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-975-084-1

Query Match 100.0%; Score 147; DB 3; Length 600;
Best Local Similarity 100.0%; Pred. No. 1.8e-09;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GMOGPAGSGWEEGSGSPPGVTPLFSP 26
Db 575 GMOGPAGSGWEEGSGSPPGVTPLFSP 600

RESULT 9
US-08-975-084-2
; Sequence 2, Application US/08975084
; Patent No. 6258780
; GENERAL INFORMATION:
; APPLICANT: SOREQ, Hermona
; APPLICANT: FRIEDMAN, Alon
; APPLICANT: SEIDMAN, Shlomo
; APPLICANT: KAUFER, Daniela
; TITLE OF INVENTION: A METHOD AND COMPOSITION FOR ENABLING
; TITLE OF INVENTION: PASSAGE THROUGH THE BLOOD-BRAIN-BARRIER
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kohn & Associates
; STREET: 30500 No. 6258780thwestern Hwy., Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: US
; ZIP: 48334
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,084
; FILING DATE: 11-NOV-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Montgomery, Ilene N.
; REGISTRATION NUMBER: 38,972
; REFERENCE/DOCKET NUMBER: 2391.00082
; TELEPHONE: (248) 539-5050
; TELEFAX: (248) 539-5055
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-975-084-2

Query Match 95.2%; Score 140; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.8e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GMOGPAGSGWEEGSGSPPGVTPLFS 25
Db 1 GMOGPAGSGWEEGSGSPPGVTPLFS 25

RESULT 10
US-07-972-032-59
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; Sequence 59, Application US/07972032
; Patent No. 5496712
; GENERAL INFORMATION:
; APPLICANT: Cappello, Joseph
; APPLICANT: Ferrari, Franco A.
; TITLE OF INVENTION: HIGH MOLECULAR WEIGHT COLLAGEN-LIKE
; TITLE OF INVENTION: PROTEIN POLYMERS
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bertram I. Rowland
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: CA 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/972,032
; FILING DATE: 19921105
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/791,960
; FILING DATE: 12-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I.
; REGISTRATION NUMBER: 20,015
; REFERENCE/DOCKET NUMBER: A-55556-1/BIR;PROP-08-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 54 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-07-972-032-59

Query Match 40.8%; Score 60; DB 1; Length 54;
Best Local Similarity 57.9%; Pred. No. 2.2;
Matches 11; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 GMOGPAGSGWEEGSGSPPG 19
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Db 1 GAQGPAGGSGRGDPGPPG 19

RESULT 11
US-08-642-255-71
; Sequence 71, Application US/08642255
; Patent No. 5773249
; GENERAL INFORMATION:
; APPLICANT: CAPPELLO, Joseph
; APPLICANT: FERRARI, Franco A.
; TITLE OF INVENTION: High Molecular Weight Collagen-Like
; TITLE OF INVENTION: Protein Polymers
; NUMBER OF SEQUENCES: 135
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/642,255
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: ROWLAND, Bertram I.
; REGISTRATION NUMBER: 20,015
; REFERENCE/DOCKET NUMBER: A55556-3/BIR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 494-8700
; TELEFAX: (415) 494-8771
; TELEX: 910 277299 FHT UR
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 54 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
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US-08-642-255-71

Query Match 40.8%; Score 60; DB 1; Length 54;
Best Local Similarity 57.9%; Pred. No. 2.2;
Matches 11; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 GMOGPAGSGWEEGSGSPPG 19
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Db 1 GAQGPAGGSGRGDPGPPG 19

RESULT 12
US-07-972-032-60
; Sequence 60, Application US/07972032
; Patent No. 5496712
; GENERAL INFORMATION:
; APPLICANT: Cappello, Joseph
; APPLICANT: Ferrari, Franco A.
; TITLE OF INVENTION: HIGH MOLECULAR WEIGHT COLLAGEN-LIKE
; TITLE OF INVENTION: PROTEIN POLYMERS
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bertram I. Rowland
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: CA 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/972,032
; FILING DATE: 19921105
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/791,960
; FILING DATE: 12-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I.
; REGISTRATION NUMBER: 20,015
; REFERENCE/DOCKET NUMBER: A-55556-1/BIR;PROP-08-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 93 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
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; NAME/KEY: Duplication
; LOCATION: 34..69
; OTHER INFORMATION: /label= internalduplica
; OTHER INFORMATION: /note= "34-42 x 2; 43-60 x 12; 61-69 x 2; 34-69 x
; OTHER INFORMATION: 4."
US-07-972-032-60

Query Match 40.8%; Score 60; DB 1; Length 93;
Best Local Similarity 57.9%; Pred. No. 3.8;
Matches 11; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 GMOGPAGSGWEEGSGSPPG 19
| | | | | | | | | | | | | | |
Db 43 GAQGPAGPGSGRGPDPGPPG 61

RESULT 13
US-07-972-032-61
; Sequence 61, Application US/07972032
; Patent No. 5496712
; GENERAL INFORMATION:
; APPLICANT: Cappello, Joseph
; APPLICANT: FERRARI, Franco A.
; TITLE OF INVENTION: HIGH MOLECULAR WEIGHT COLLAGEN-LIKE
; TITLE OF INVENTION: PROTEIN POLYMERS
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bertram I. Rowland
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: CA 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/972,032
; FILING DATE: 19921105
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/791,960
; FILING DATE: 12-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I.
; REGISTRATION NUMBER: 20,015
; REFERENCE/DOCKET NUMBER: A-55556-1/BIR;PROP-08-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 93 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Duplication
; LOCATION: 34..69
; OTHER INFORMATION: /label= internalduplica
; OTHER INFORMATION: /note= "34-42 x 2; 43-60 x 6; 61-69 x 2; 34-69 x
; OTHER INFORMATION: 4."
US-07-972-032-61

Query Match 40.8%; Score 60; DB 1; Length 93;
Best Local Similarity 57.9%; Pred. No. 3.8;
Matches 11; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 GMOGPAGSGWEEGSGSPPG 19
| | | | | | | | | | | | | | |
Db 43 GAQGPAGPGSGRGPDPGPPG 61
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RESULT 14
US-08-642-255-73
; Sequence 73, Application US/08642255
; Patent No. 5773249
; GENERAL INFORMATION:
; APPLICANT: CAPPELLO, Joseph
; APPLICANT: FERRARI, Franco A.
; TITLE OF INVENTION: High Molecular Weight Collagen-Like
; TITLE OF INVENTION: Protein Polymers
; NUMBER OF SEQUENCES: 135
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/642,255
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: ROWLAND, Bertram I.
; REGISTRATION NUMBER: 20,015
; REFERENCE/DOCKET NUMBER: A55556-3/BIR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 494-8700
; TELEFAX: (415) 494-8771
; TELEX: 910 277299 FHT UR
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 633 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-642-255-73

Query Match 40.8%; Score 60; DB 1; Length 633;
Best Local Similarity 57.9%; Pred. No. 26;
Matches 11; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 GMOGPAGSGWEEGSGSPPG 19
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Db 52 GAQGPAGPGSGRGPDPGPPG 70

RESULT 15
US-08-642-255-72
; Sequence 72, Application US/08642255
; Patent No. 5773249
; GENERAL INFORMATION:
; APPLICANT: CAPPELLO, Joseph
; APPLICANT: FERRARI, Franco A.
; TITLE OF INVENTION: High Molecular Weight Collagen-Like
; TITLE OF INVENTION: Protein Polymers
; NUMBER OF SEQUENCES: 135
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/642,255
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: ROWLAND, Bertram I.
; REGISTRATION NUMBER: 20,015
; REFERENCE/DOCKET NUMBER: A55556-3/BIR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 494-8700
; TELEFAX: (415) 494-8771
; TELEX: 910 277299 FHT UR
; INFORMATION FOR SEQ ID NO: 72:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1065 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-642-255-72

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Query Match      40.8%; Score 60; DB 1; Length 1065;
Best Local Similarity 57.9%; Pred. No. 44;
Matches 11; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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QY      1 GMQGPAGSGWEEGSGSPPG 19
         |||||
Db      52 GAQGPAGPGSGRGDPGPPG 70

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Search completed: October 29, 2005, 01:05:21
Job time : 43 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 29, 2005, 01:03:40 ; Search time 165 Seconds
(without alignments)
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Title: US-09-980-263-1

Perfect score: 147
Sequence: 1 GMOGPAGSGWEEGSGSPPGVTPLFSP 26

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1865214 seqs, 418043040 residues

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
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12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
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19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	147	100.0	26	10 US-09-998-042-1	Sequence 1, Appli
2	147	100.0	37	10 US-09-998-042-6	Sequence 6, Appli
3	147	100.0	53	10 US-09-998-042-7	Sequence 7, Appli
4	68	46.3	105	16 US-10-425-115-356384	Sequence 356384,
5	61.5	41.8	157	16 US-10-425-115-274774	Sequence 274774,
6	61.5	41.8	575	15 US-10-276-774-1845	Sequence 1845, Ap
7	61	41.5	138	16 US-10-425-115-221226	Sequence 221226,
8	60	40.8	334	18 US-10-820-155-131	Sequence 131, App
9	60	40.8	334	18 US-10-820-155-133	Sequence 133, App
10	60	40.8	528	16 US-10-425-115-250621	Sequence 250621,
11	60	40.8	534	15 US-10-425-114-70635	Sequence 70635, A

12	60	40.8	1466	15	US-10-402-089-4	Sequence 4, Appli
13	60	40.8	1466	15	US-10-402-089-6	Sequence 6, Appli
14	60	40.8	1466	15	US-10-402-072A-4	Sequence 4, Appli
15	60	40.8	1466	15	US-10-402-072A-6	Sequence 6, Appli
16	59	40.1	78	15	US-10-424-599-194897	Sequence 194897,
17	59	40.1	102	16	US-10-425-115-250617	Sequence 250617,
18	59	40.1	155	16	US-10-767-701-60190	Sequence 60190, A
19	59	40.1	598	16	US-10-425-115-250618	Sequence 250618,
20	59	40.1	603	16	US-10-437-963-167449	Sequence 167449,
21	58.5	39.8	72	18	US-10-756-149-4761	Sequence 4761, Ap
22	58.5	39.8	136	16	US-10-425-115-271420	Sequence 271420,
23	58	39.5	185	16	US-10-437-963-121283	Sequence 121283,
24	58	39.5	185	16	US-10-437-963-182893	Sequence 182893,
25	58	39.5	226	15	US-10-104-047-2316	Sequence 2316, Ap
26	58	39.5	251	15	US-10-094-749-2497	Sequence 2497, Ap
27	58	39.5	393	14	US-10-210-951-34	Sequence 34, Appl
28	58	39.5	393	14	US-10-211-884-34	Sequence 34, Appl
29	58	39.5	393	15	US-10-211-858-34	Sequence 34, Appl
30	58	39.5	393	15	US-10-094-749-2518	Sequence 2518, Ap
31	58	39.5	393	20	US-11-052-503-2	Sequence 2, Appli
32	58	39.5	638	13	US-10-001-887-108	Sequence 108, App
33	58	39.5	638	15	US-10-138-588-42	Sequence 42, Appl
34	58	39.5	638	17	US-10-958-863-108	Sequence 108, App
35	58	39.5	703	14	US-10-219-449-4	Sequence 4, Appli
36	58	39.5	703	17	US-10-958-858-4	Sequence 4, Appli
37	58	39.5	717	14	US-10-219-449-2	Sequence 2, Appli
38	58	39.5	717	17	US-10-958-858-2	Sequence 2, Appli
39	58	39.5	733	15	US-10-138-588-40	Sequence 40, Appl
40	57.5	39.1	280	9	US-09-823-038A-18	Sequence 18, Appl
41	57	38.8	103	16	US-10-425-115-207493	Sequence 207493,
42	57	38.8	133	16	US-10-425-115-257391	Sequence 257391,
43	57	38.8	386	16	US-10-437-963-168962	Sequence 168962,
44	57	38.8	407	15	US-10-425-114-55894	Sequence 55894, A
45	57	38.8	674	9	US-09-925-299-979	Sequence 979, App

ALIGNMENTS

RESULT 1
US-09-998-042-1
; Sequence 1, Application US/09998042
; Publication No. US20030036632A1
; GENERAL INFORMATION:
; APPLICANT: YISSUM RESEARCH DEVELOPMENT COMPANY OF THE HEBREW
; TITLE OF INVENTION: ACETYLCHOLINESTERASE-DERIVED PEPTIDE AND USES THEREOF
; FILE REFERENCE: 7811/WO/99
; CURRENT APPLICATION NUMBER: US/09/998,042
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 26
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-998-042-1

Query Match 100.0%; Score 147; DB 10; Length 26;
Best Local Similarity 100.0%; Pred. No. 1e-09;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GMOGPAGSGWEEGSGSPPGVTPLFSP 26
|||
Db 1 GMOGPAGSGWEEGSGSPPGVTPLFSP 26

RESULT 2
US-09-998-042-6
; Sequence 6, Application US/09998042
; Publication No. US20030036632A1
; GENERAL INFORMATION:
; APPLICANT: YISSUM RESEARCH DEVELOPMENT COMPANY OF THE HEBREW
; TITLE OF INVENTION: ACETYLCHOLINESTERASE-DERIVED PEPTIDE AND USES THEREOF

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; FILE REFERENCE: 7811/WO/99
; CURRENT APPLICATION NUMBER: US/09/998,042
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 6
; LENGTH: 37
; TYPE: PRT
; ORGANISM: homo sapiens
; US-09-998-042-6

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Query Match	100.0%;	Score 147;	DB 10;	Length 37;
Best Local Similarity	100.0%;	Pred. No. 1.4e-09;		
Matches 26;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	1	GMQPGAGSGWEEGSGPPGVTPLFSP	26
D _b	12	GMQPGAGSGWEEGSGPPGVTPLFSP	37

RESULT 3

US-09-998-042-7
; Sequence 7, Application US/09998042
; Publication No. US20030036632A1
: GENERAL INFORMATION:

APPLICANT: YISSUM RESEARCH DEVELOPMENT COMPANY OF THE HEBREW
TITLE OF INVENTION: ACETYLCHOLINESTERASE-DERIVED PEPTIDE AND
FILE REFERENCE: 7811/WO/99
CURRENT APPLICATION NUMBER: US/09/998,042
CURRENT FILING DATE: 2002-07-02

```

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:arp-two hybrid
; OTHER INFORMATION: screen peptide
US-09-998-042-7

```

```
Query Match      100.0%; Score 147; DB 10; Length 53;
Best Local Similarity 100.0%; Pred. No. 2e-09;
Matches 26: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY	1	28	53
	GMQGPAGSGWEEGSGSPPGVTPLFSP	GMQGPAGSGWEEGSGSPPGVTPLFSP	GMQGPAGSGWEEGSGSPPGVTPLFSP

RESULT 4

US-10-425-115-356384
; Sequence 356384, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.
 APPLICANT: Kovalic, David K.
 APPLICANT: Zhou, Yihua
 APPLICANT: Cao, Yongwei
 TITLE OF INVENTION: Plants
 TITLE OF INVENTION: Plants
 FILE REFERENCE: 38-21(53222)B
 CURRENT APPLICATION NUMBER: US/10/425,115
 CURRENT FILING DATE: 2003-04-28
 NUMBER OF SEQ ID NOS: 369326

```

; NAME/KEY: unsure
; LOCATION: (1)..(105)
; OTHER INFORMATION: unsure at all Xaa locations

```

```

; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_88191C.1.pcp
US-10-425-115-356384

```

Query Match 46.3%; Score 68; DB 16; Length 105;
Best Local Similarity 61.1%; Pred. No. 3.3;
Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 G M Q C P A G S G W E E G S G S P P 18
 | : | | | | | | : | |
Db 80 G T R G P G S G W P S P S G N P P 97

RESULT 5

US-10-425-115-274774
; Sequence 274774, Application US/10425115
; Publication No. US20040214272A1

; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants
 ; FILE REFERENCE: 38-21(53222)B
 ; CURRENT APPLICATION NUMBER: US/10/425,115
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 369326
 ; SEQ ID NO 274774

NAME/KEY: unsure
LOCATION: (1) (157)

OTHER INFORMATION: Clone ID: MRT4577_182182C.1.pcp
US-10-425-115-274774

Query Match 41.8%; Score 61.5; DB 16; Length 157;
Best Local Similarity 65.0%; Pred. No. 26;
Matches 13; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

QY 3 QGPAGSGWEEGSGSPGVTP 22
 : || | | | | | : | | |
pb 132 KGP-GSGGEETGWPPGPPP 150

RESULT 6

US-10-276-774-1845
; Sequence 1845, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:

```

; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang, Y, Tom et al
; TITLE OF INVENTION: No. US20040053245A1e1 Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: US/10/276,774
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 1845

```

```

; NAME/KEY: misc_feature
; LOCATION: (1) : (575)

```

OTHER INFORMATION: Xaa = any amino acid or nothing
US-10-276-774-1845

Query Match 41.8%; Score 61.5; DB 15; Length 575;
Best Local Similarity 56.5%; Pred. No. 88;
Matches 13; Conservative 2; Mismatches 7; Indels 1; Gaps 1;

QY 1 GMSG-PAGSGWEEGSGSPPGVTP 22
DB 421 GGQGLPEGWGLEKGEGLPPGIPP 443

RESULT 7

US-10-425-115-221226
; Sequence 221226, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 221226
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(138)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_133350C.1.pep
; US-10-425-115-221226

Query Match 41.5%; Score 61; DB 16; Length 138;
Best Local Similarity 52.4%; Pred. No. 26;
Matches 11; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

QY 4 GPAGS--GWEEGSGSPPGVTP 22
DB 95 GPMGTGLGWRPGAGGPPGPIP 115

RESULT 8

US-10-820-155-131
; Sequence 131, Application US/10820155
; Publication No. US20050137126A1
; GENERAL INFORMATION:
; APPLICANT: NatImmune A/S
; APPLICANT: Weillguny, Dietmar
; APPLICANT: Jensenius, Jens Christian
; APPLICANT: Kongerslev, Leif
; APPLICANT: Matthiesen, Finn
; TITLE OF INVENTION: Treatment of SARS in individuals
; FILE REFERENCE: P 774 US00
; CURRENT APPLICATION NUMBER: US/10/820,155
; CURRENT FILING DATE: 2004-04-08
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 131
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-820-155-131

Query Match 40.8%; Score 60; DB 18; Length 334;
Best Local Similarity 60.0%; Pred. No. 78;
Matches 12; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 GMSG-PAGSGWEEGSGSPPGV 20
DB 77 GKMG-PAGSKGEPGTMGPPGV 96

RESULT 9

US-10-820-155-133
; Sequence 133, Application US/10820155
; Publication No. US20050137126A1
; GENERAL INFORMATION:
; APPLICANT: NatImmune A/S
; APPLICANT: Weillguny, Dietmar
; APPLICANT: Jensenius, Jens Christian
; APPLICANT: Kongerslev, Leif
; APPLICANT: Matthiesen, Finn
; TITLE OF INVENTION: Treatment of SARS in individuals
; FILE REFERENCE: P 774 US00
; CURRENT APPLICATION NUMBER: US/10/820,155
; CURRENT FILING DATE: 2004-04-08
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 133
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-820-155-133

Query Match 40.8%; Score 60; DB 18; Length 334;
Best Local Similarity 60.0%; Pred. No. 78;
Matches 12; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 GMSG-PAGSGWEEGSGSPPGV 20
DB 77 GKMG-PAGSKGEPGTMGPPGV 96

RESULT 10

US-10-425-115-250621
; Sequence 250621, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 250621
; LENGTH: 528
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_160154C.1.pep
; US-10-425-115-250621

Query Match 40.8%; Score 60; DB 16; Length 528;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 2; Mismatches 10; Indels 2; Gaps 1;

QY 1 GMSG--GSGWEEGSGSPPGVTPFLFSP 26
DB 7 GRAGGAIKRGWKYSGFVDGVFPVLPSP 34

RESULT 11

US-10-425-114-70635
; Sequence 70635, Application US/10425114
; Publication No. US20040034888A1

```
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 70635
; LENGTH: 534
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLB73046D03_FLI.pep
US-10-425-114-70635
```

```
Query Match 40.8%; Score 60; DB 15; Length 534;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
Matches 14; Conservative 2; Mismatches 10; Indels 2; Gaps 1;
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```
QY 1 GMOGPA--GSGWEEGSGSPPGVTPLFSP 26
| | | | | | | | | | | | | | | |
Db 13 GRAGGAIKRGWKYSGFVDGVFPVLSP 40
```

```
•RESULT 12
US-10-402-089-4
; Sequence 4, Application US/10402089
; Publication No. US20040005663A1
; GENERAL INFORMATION:
; APPLICANT: Bell, Marcum P.
; APPLICANT: Neff, Thomas B.
; APPLICANT: Polarek, James W.
; APPLICANT: Seeley, Todd W.
; TITLE OF INVENTION: PORCINE COLLAGENS AND GELATINS
; FILE REFERENCE: FP0402.3 CON
; CURRENT APPLICATION NUMBER: US/10/402,089
; CURRENT FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: US 09/709,700
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 1466
; TYPE: PRT
; ORGANISM: Bos Taurus
US-10-402-089-4
```

```
Query Match 40.8%; Score 60; DB 15; Length 1466;
Best Local Similarity 57.1%; Pred. No. 3.1e+02;
Matches 12; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
```

```
QY 1 GMOGPAGSGWEEGSGSPPGVT 21
| | | | | | | | | | | | | |
Db 603 GPQGPAGKNGETGPQGPPT 623
```

```
RESULT 13
US-10-402-089-6
; Sequence 6, Application US/10402089
; Publication No. US20040005663A1
; GENERAL INFORMATION:
; APPLICANT: Bell, Marcum P.
; APPLICANT: Neff, Thomas B.
; APPLICANT: Polarek, James W.
; APPLICANT: Seeley, Todd W.
; TITLE OF INVENTION: PORCINE COLLAGENS AND GELATINS
; FILE REFERENCE: FP0402.3 CON
```

```
; CURRENT APPLICATION NUMBER: US/10/402,089
; CURRENT FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: US 09/709,700
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 1466
; TYPE: PRT
; ORGANISM: Sus scrofa
US-10-402-089-6
```

```
Query Match 40.8%; Score 60; DB 15; Length 1466;
Best Local Similarity 57.1%; Pred. No. 3.1e+02;
Matches 12; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
```

```
QY 1 GMOGPAGSGWEEGSGSPPGVT 21
| | | | | | | | | | | | | |
Db 603 GPQGPAGKNGETGPQGPPT 623
```

```
RESULT 14
US-10-402-072A-4
; Sequence 4, Application US/10402072A
; Publication No. US20040018592A1
; GENERAL INFORMATION:
; APPLICANT: Bell, Marcum P.
; APPLICANT: Neff, Thomas B.
; APPLICANT: Polarek, James W.
; APPLICANT: Seeley, Todd W.
; TITLE OF INVENTION: BOVINE COLLAGENS AND GELATINS
; FILE REFERENCE: FP0402.2 CON
; CURRENT APPLICATION NUMBER: US/10/402,072A
; CURRENT FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: US 09/709,700
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 1466
; TYPE: PRT
; ORGANISM: Bos Taurus
US-10-402-072A-4
```

```
Query Match 40.8%; Score 60; DB 15; Length 1466;
Best Local Similarity 57.1%; Pred. No. 3.1e+02;
Matches 12; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
```

```
QY 1 GMOGPAGSGWEEGSGSPPGVT 21
| | | | | | | | | | | | | |
Db 603 GPQGPAGKNGETGPQGPPT 623
```

```
RESULT 15
US-10-402-072A-6
; Sequence 6, Application US/10402072A
; Publication No. US20040018592A1
; GENERAL INFORMATION:
; APPLICANT: Bell, Marcum P.
; APPLICANT: Neff, Thomas B.
; APPLICANT: Polarek, James W.
; APPLICANT: Seeley, Todd W.
; TITLE OF INVENTION: BOVINE COLLAGENS AND GELATINS
; FILE REFERENCE: FP0402.2 CON
; CURRENT APPLICATION NUMBER: US/10/402,072A
; CURRENT FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: US 09/709,700
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 1466
; TYPE: PRT
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; ORGANISM: Sus scrofa
US-10-402-072A-6

Query Match 40.8%; Score 60; DB 15; Length 1466;
Best Local Similarity 57.1%; Pred. No. 3.1e+02;
Matches 12; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 GMQGPAGSGWEEGSGSPPGVT 21
| | | | | | | | | | | | | | | | | | | | | |
Db 603 GPQGPAGKNGETGPQGPPT 623

Search completed: October 29, 2005, 01:18:08
Job time : 166 secs